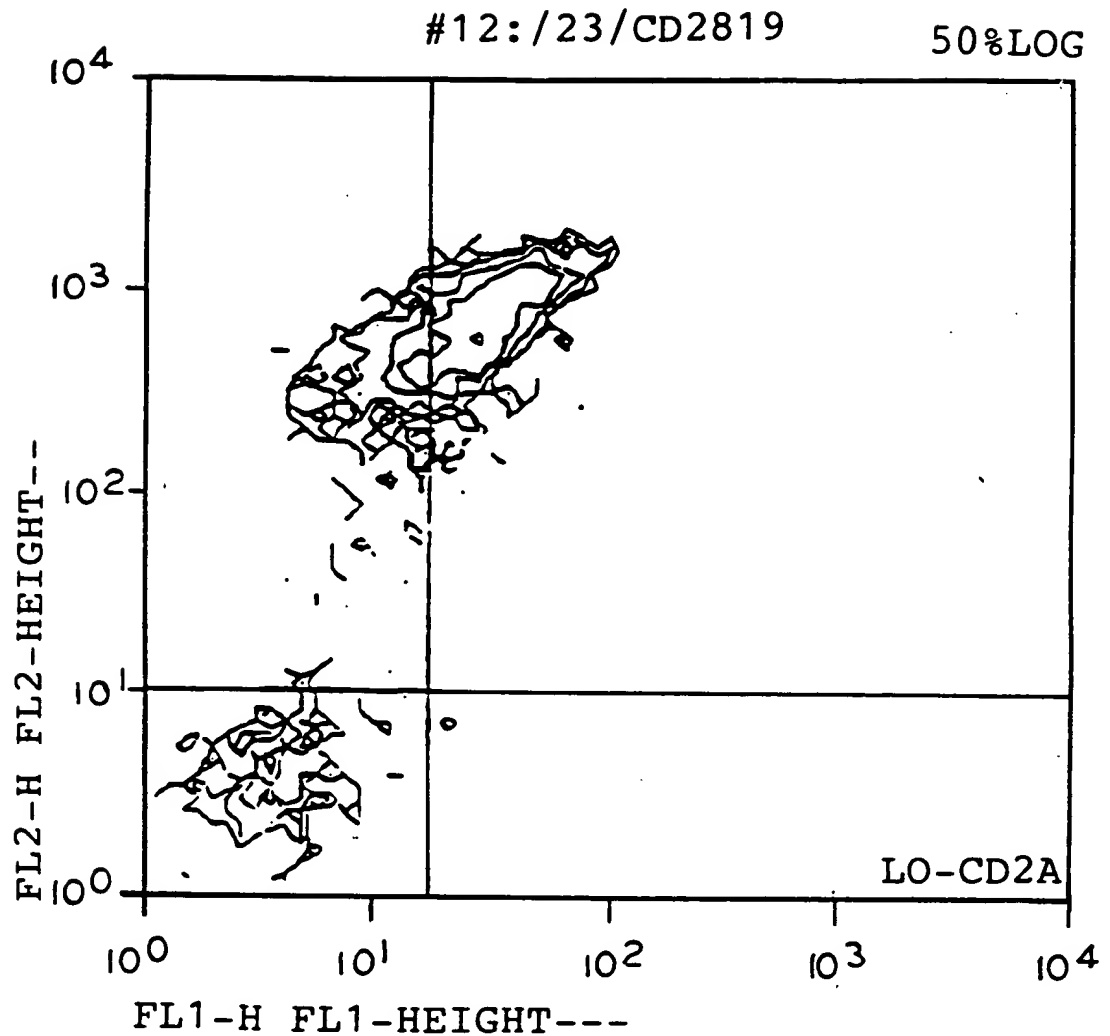


1 / 53

FIG. 1



#12:/23/CD2019

---QUAD STATS---

FILE: #12:/23/CD2019 SAMPLE: 059

DATE: 9/24/92 GATE G1-R1

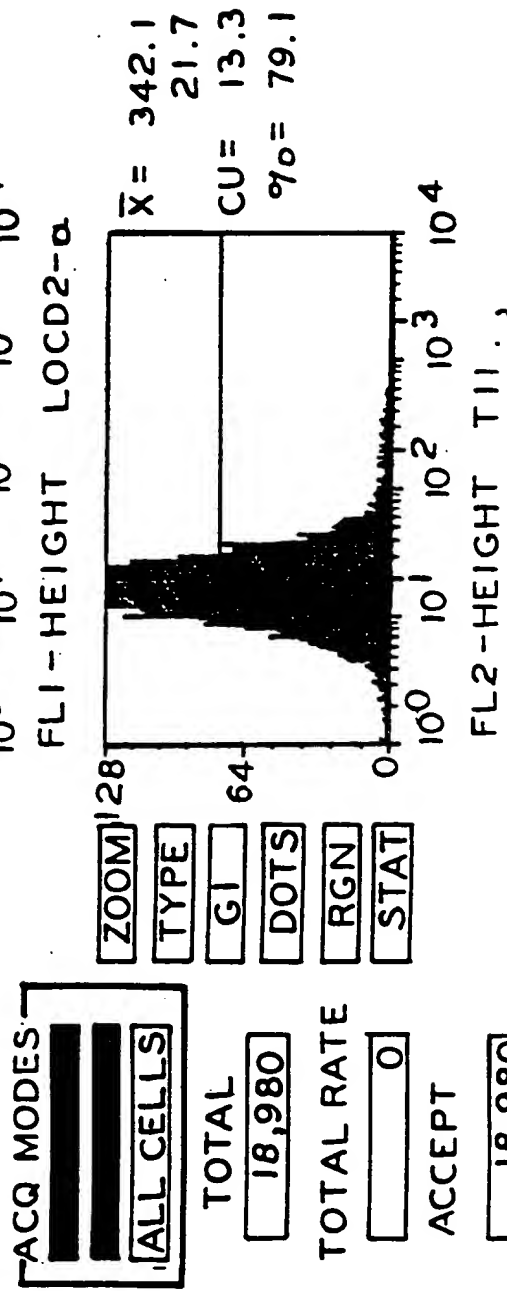
PARAMETER: FL1-H (LOG) FL2-H (LOG) QUAD

LOCATION: 17.15.9

TOTAL=	5000	GATED=	L290		
QUAD	EVENTS	% GATED	%TOTAL	X MEAN	Y MEAN
IUL	299	23.18	3.98	11.41	284.69
2UR	851	65.97	17.02	32.70	630.65
3LL	135	10.47	2.70	4.08	3.31
4LR	5	0.39	0.10	25.11	6.54

862040-22095060

ACO CMD INST-CTRL GATES FORMAT PROTO SAVE



TOTAL

18,980

TOTAL RATE

0

ACCEPT

18,980

ELAPSED TIME

00:00:48

FIG. 2A

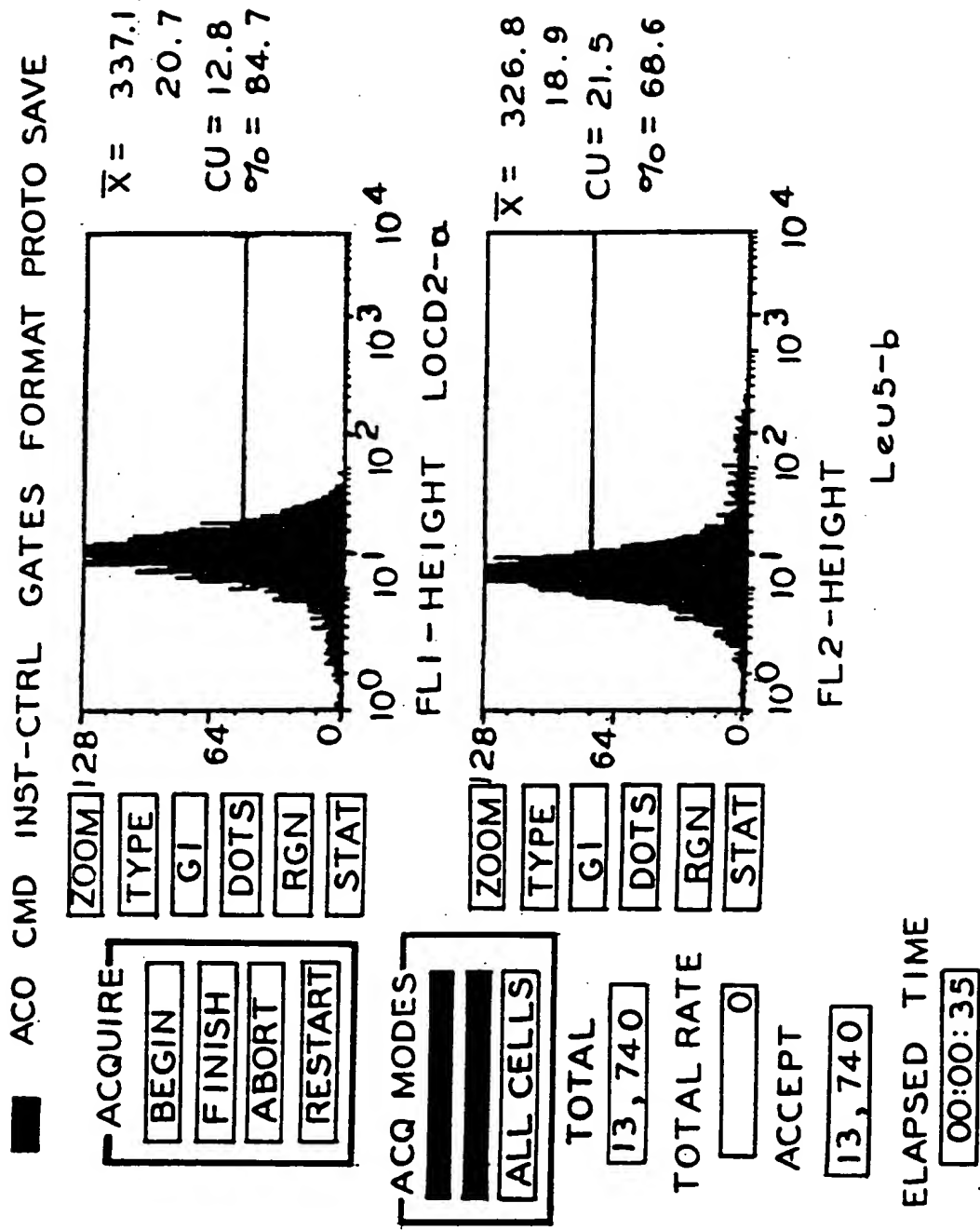


FIG. 2B

FIG. 3A

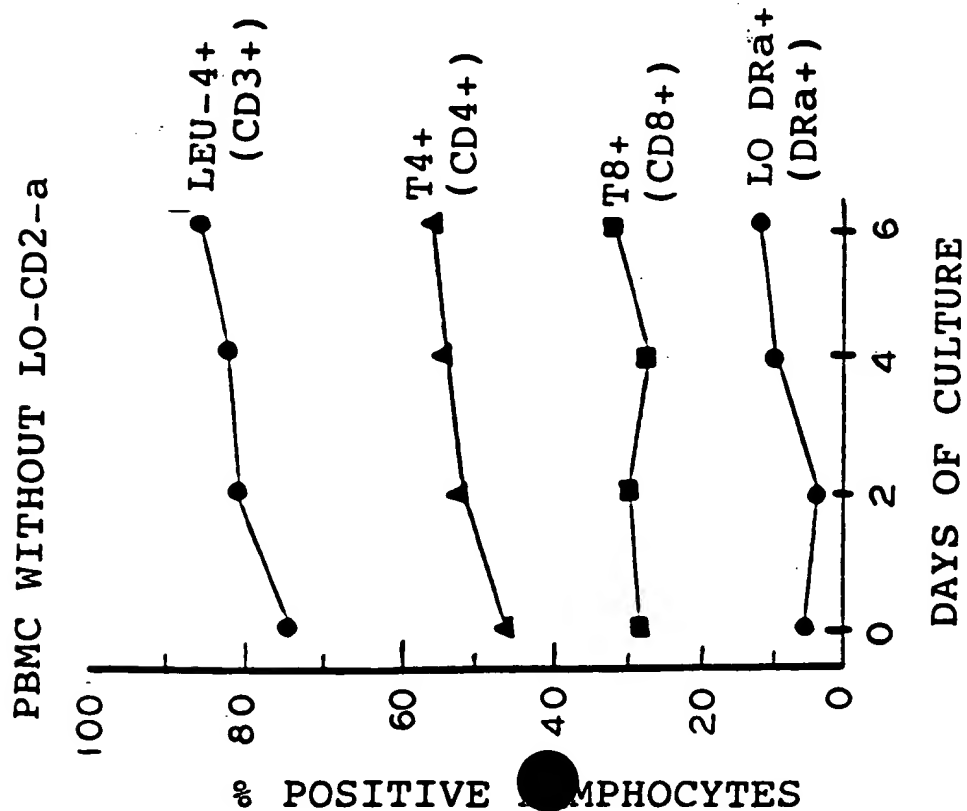


FIG. 3B

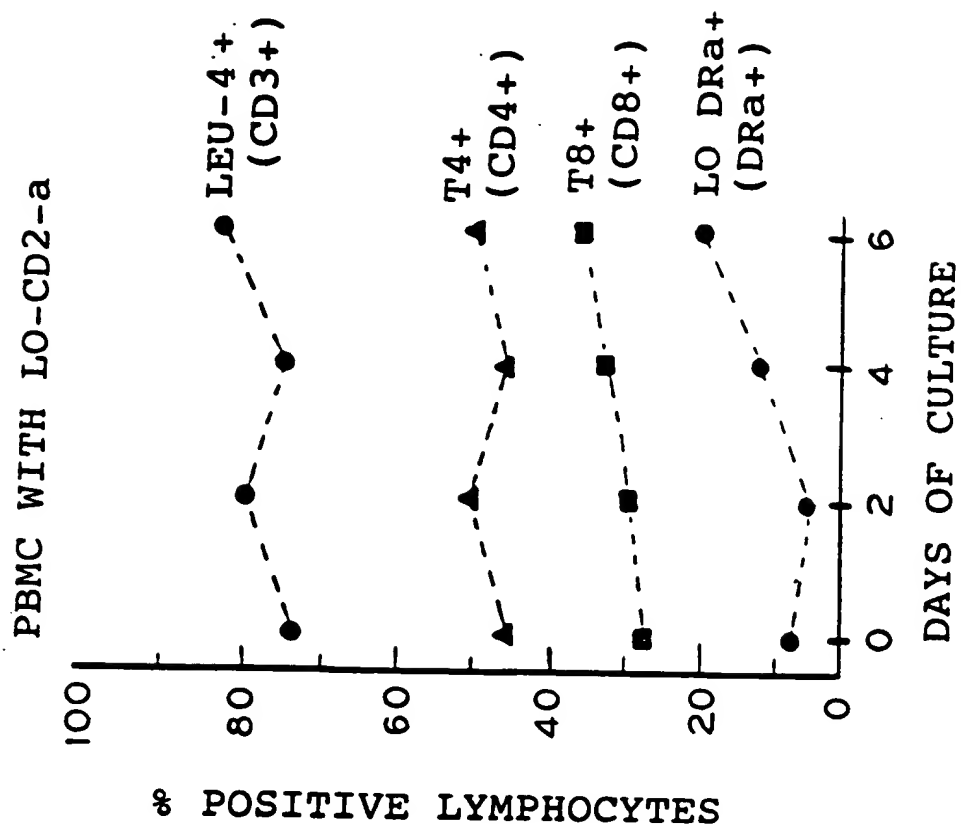
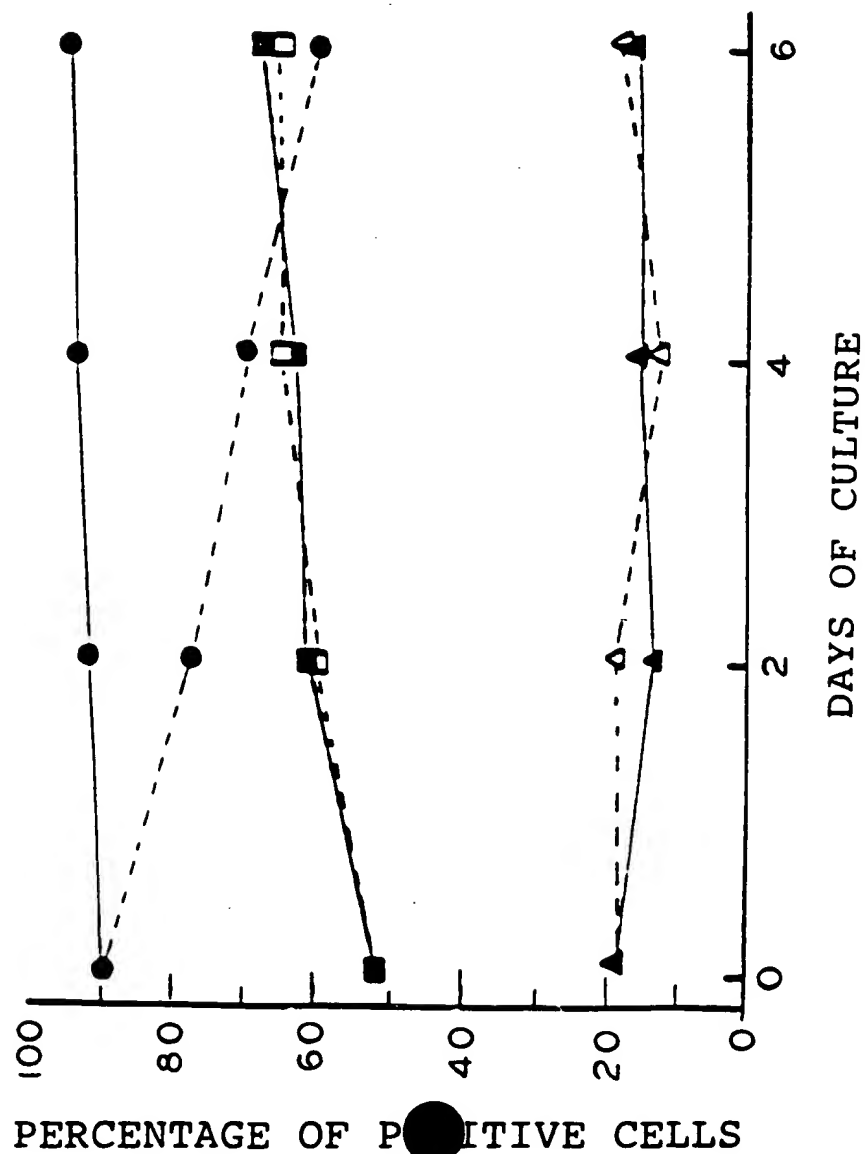


FIG. 4

PBMC: PHENOTYPICAL ANALYSIS



5 / 53

6 / 53

FIG. 5A

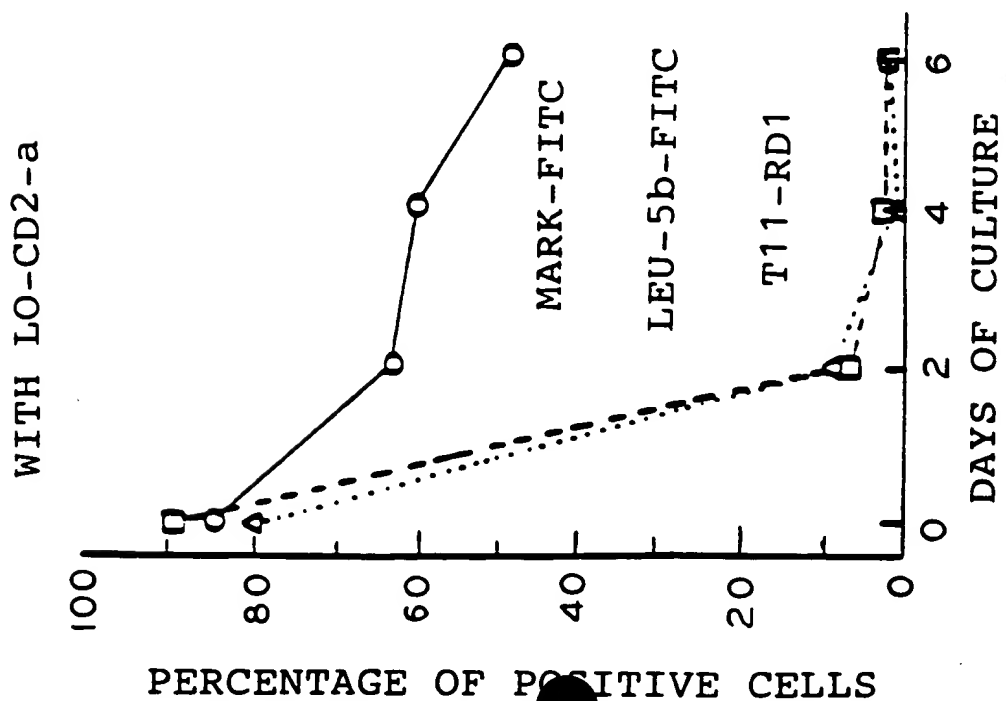
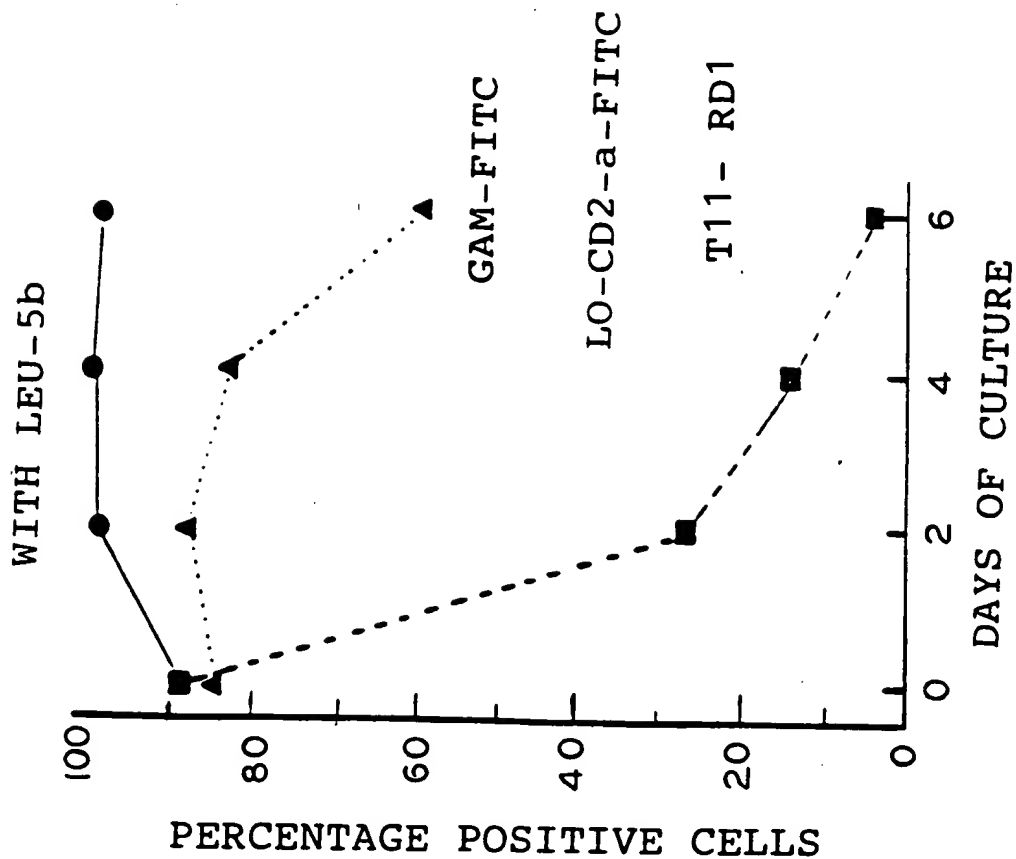


FIG. 5B



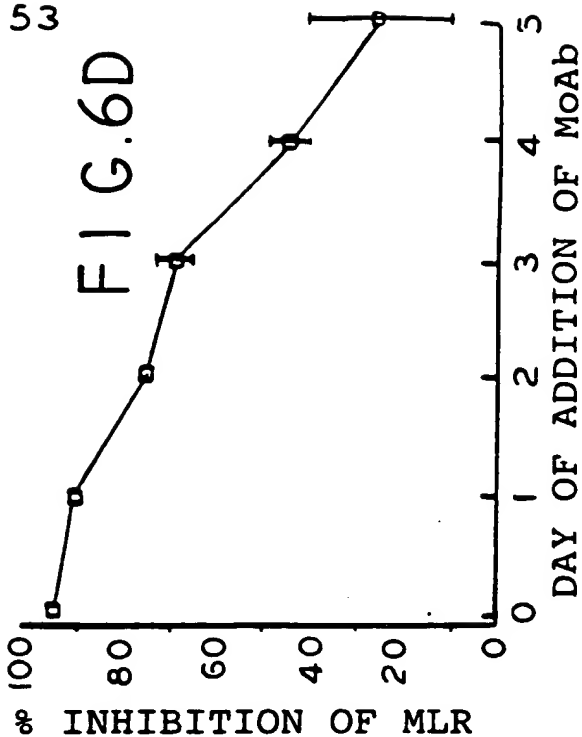
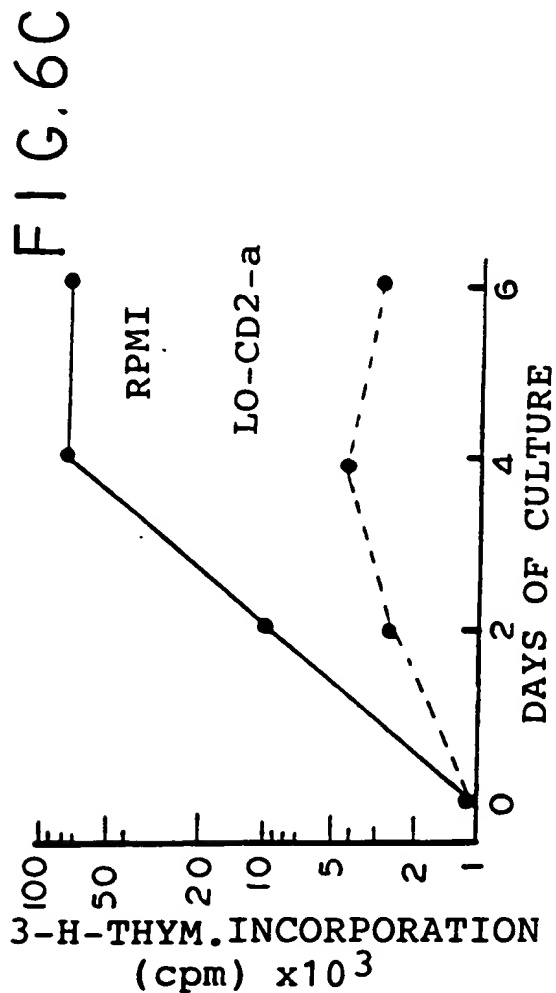
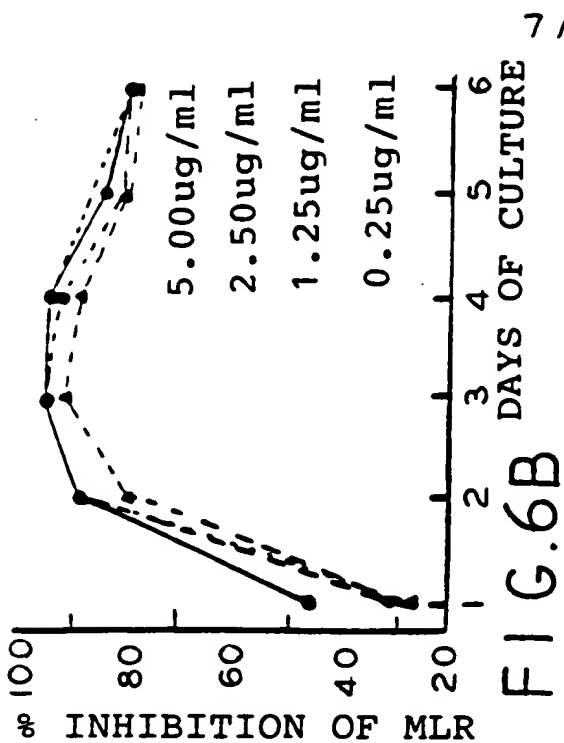
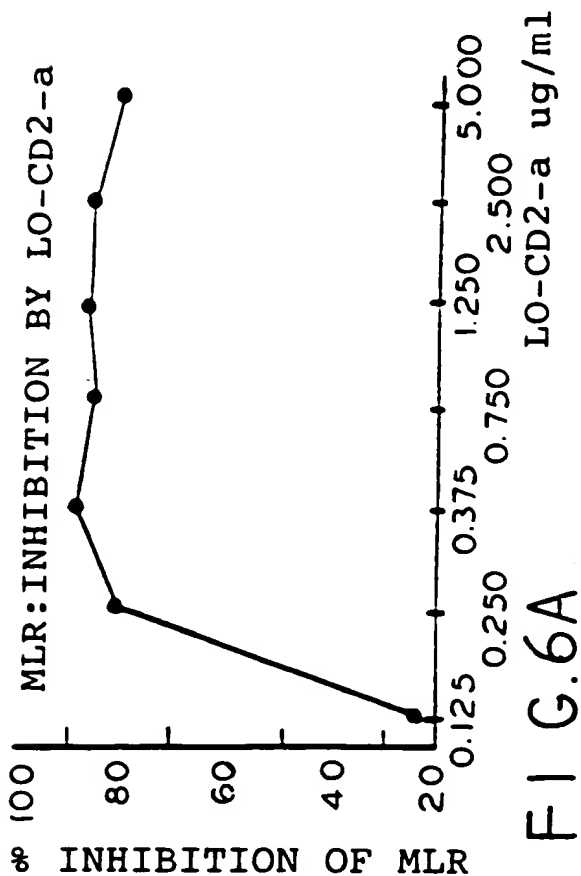


FIG. 7A

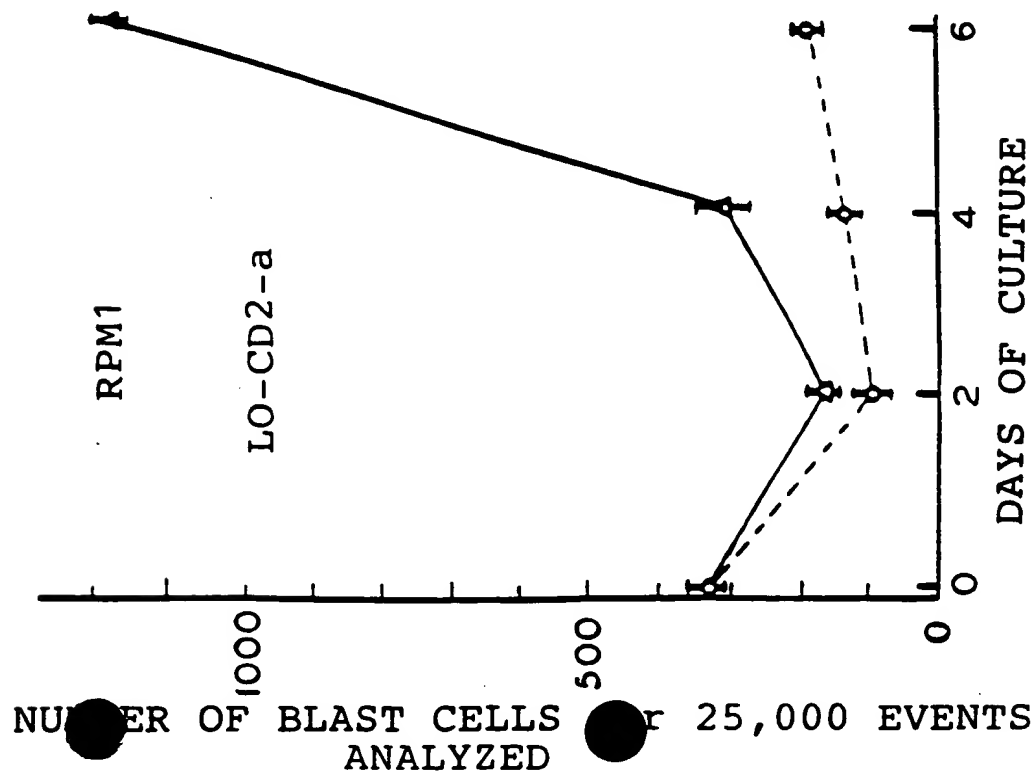
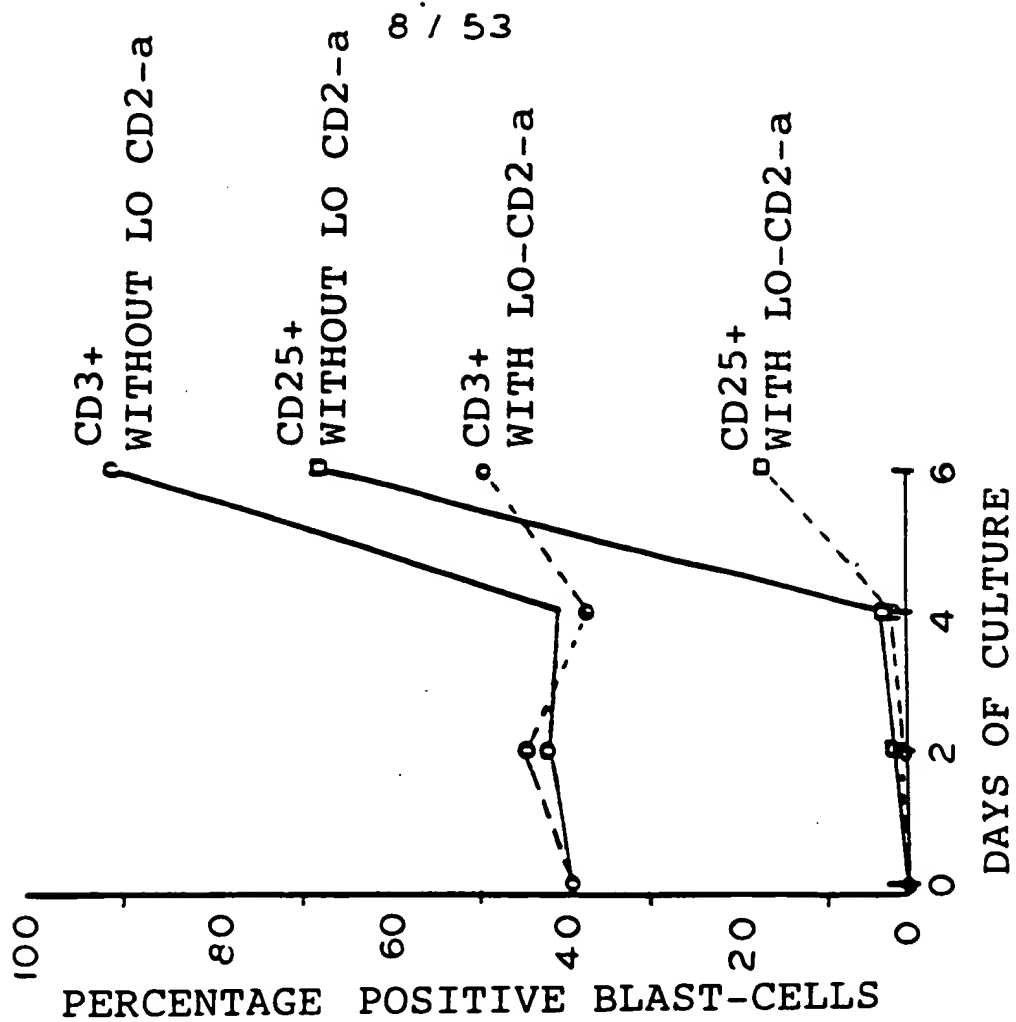
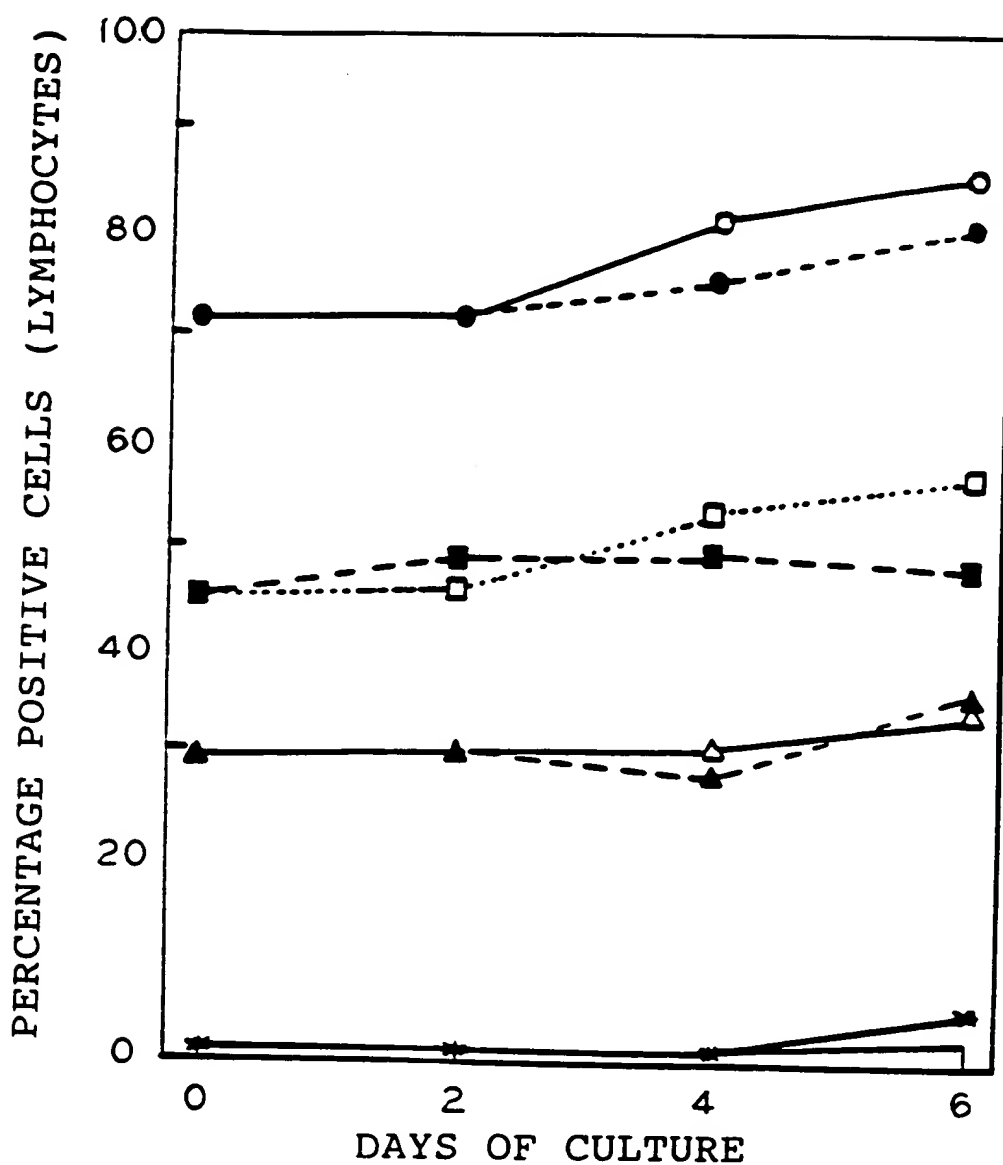


FIG. 7B



8 / 53

FIG. 8A



CD3+ (-MoAb) CD3+ (-MoAb)

CD8+ (-MoAb) CD8+ (+MoAb)

CD4+ (-MoAb) CD4+ (-MoAb)

CD25+ (-MoAb) CD25+ (+MoAb)

10 / 53

FIG. 8B

MLC:LEU-56+(CD2+) CELLS

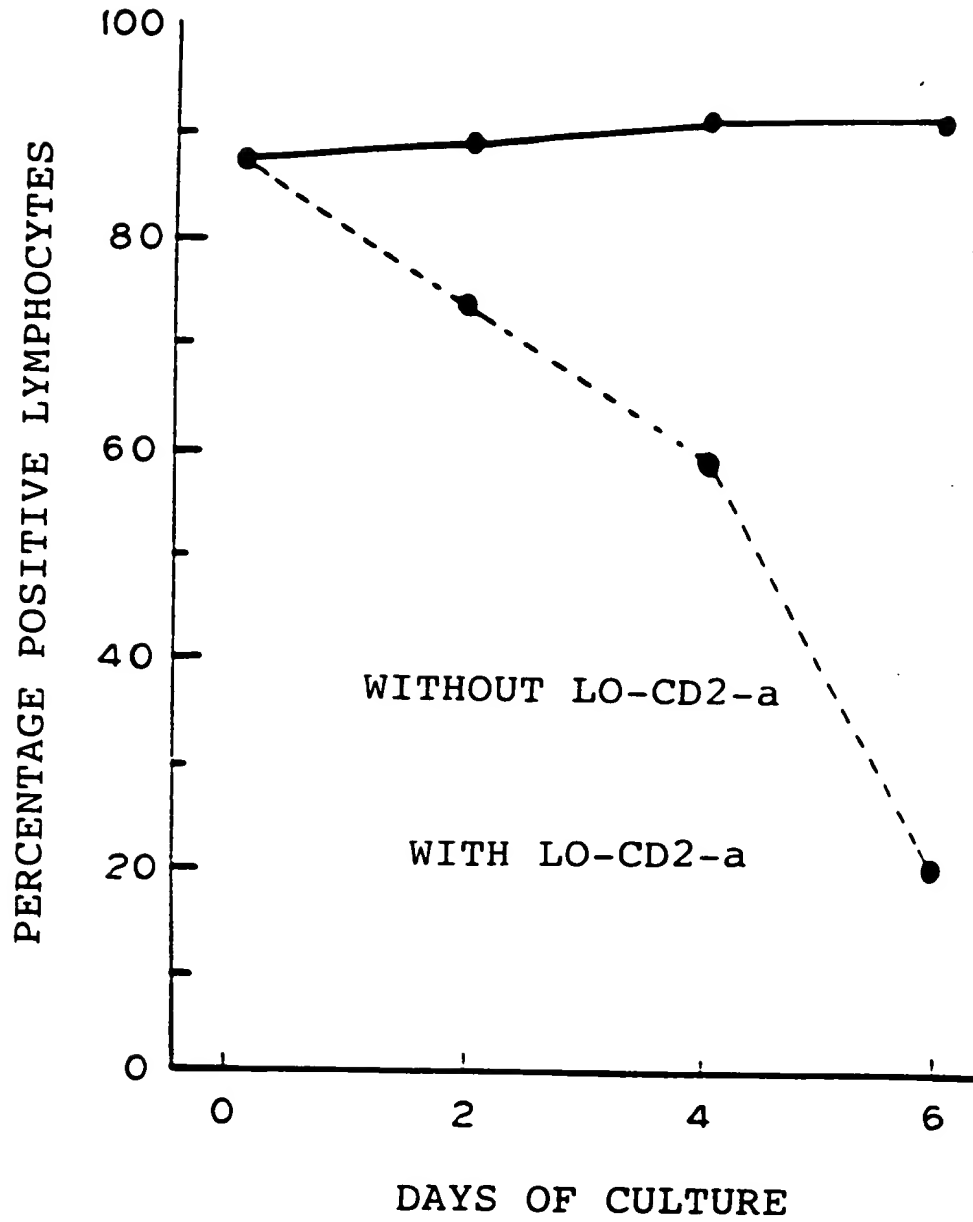
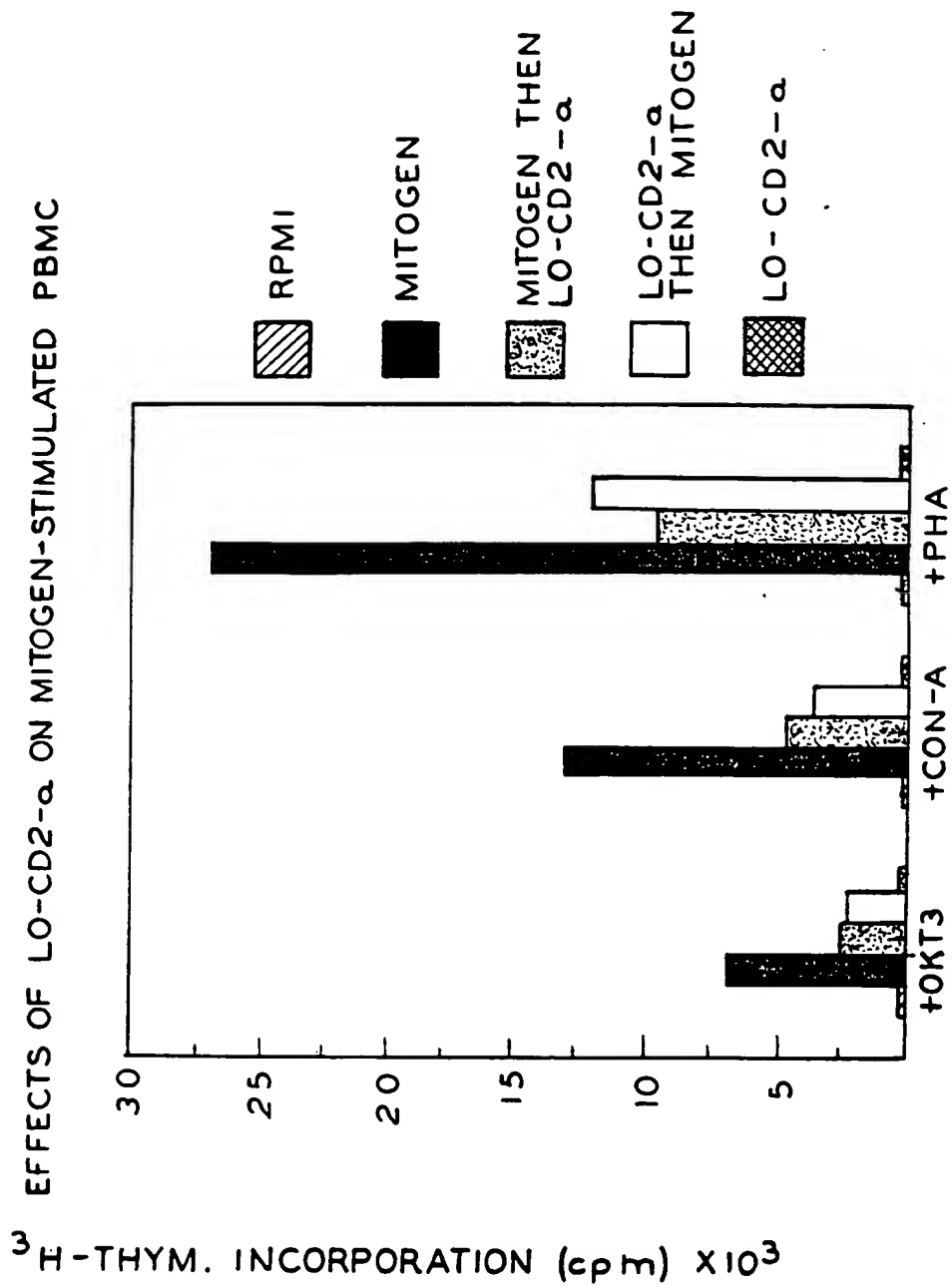


FIG. 9



12 / 53

FIG. 10

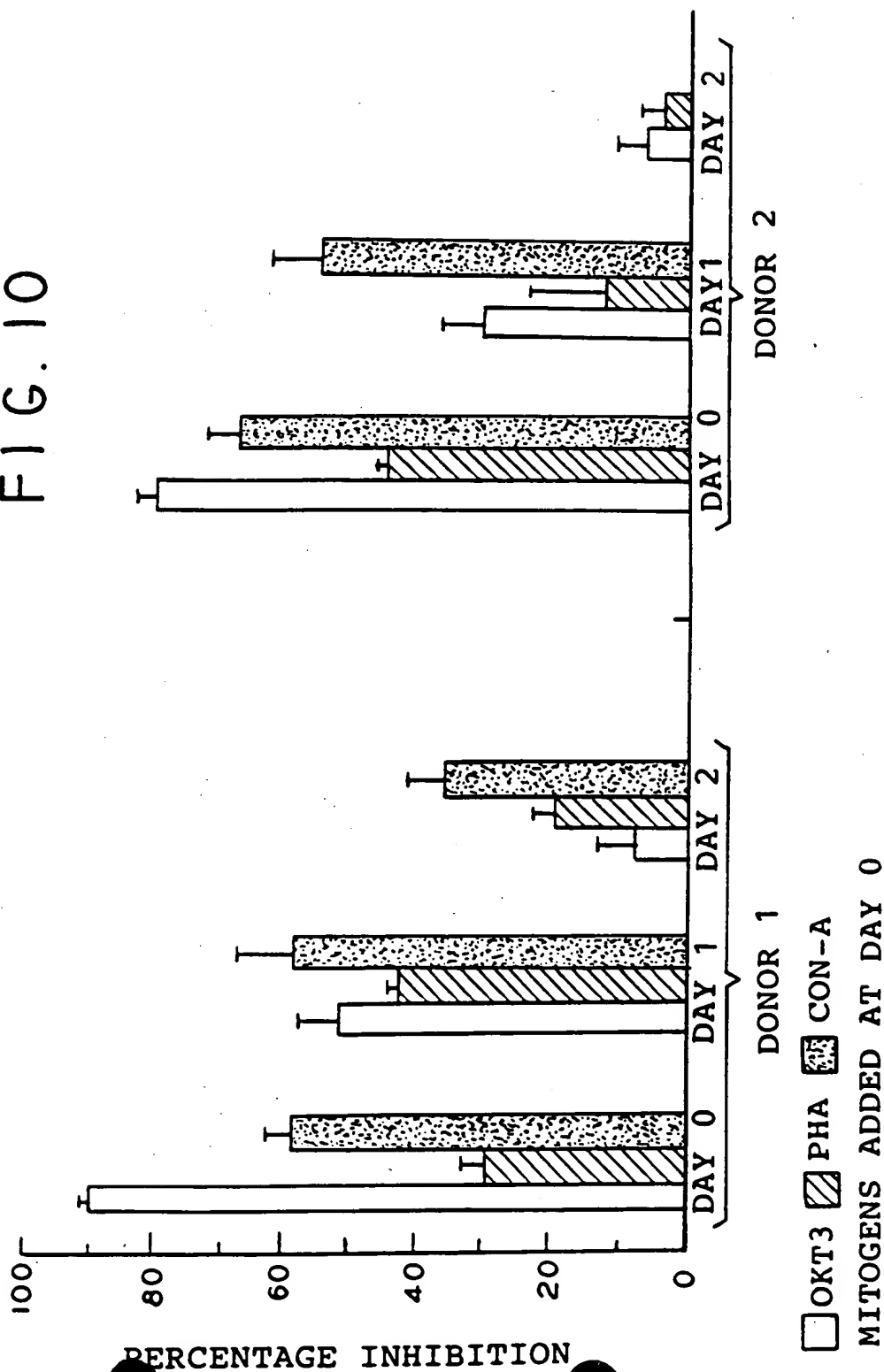
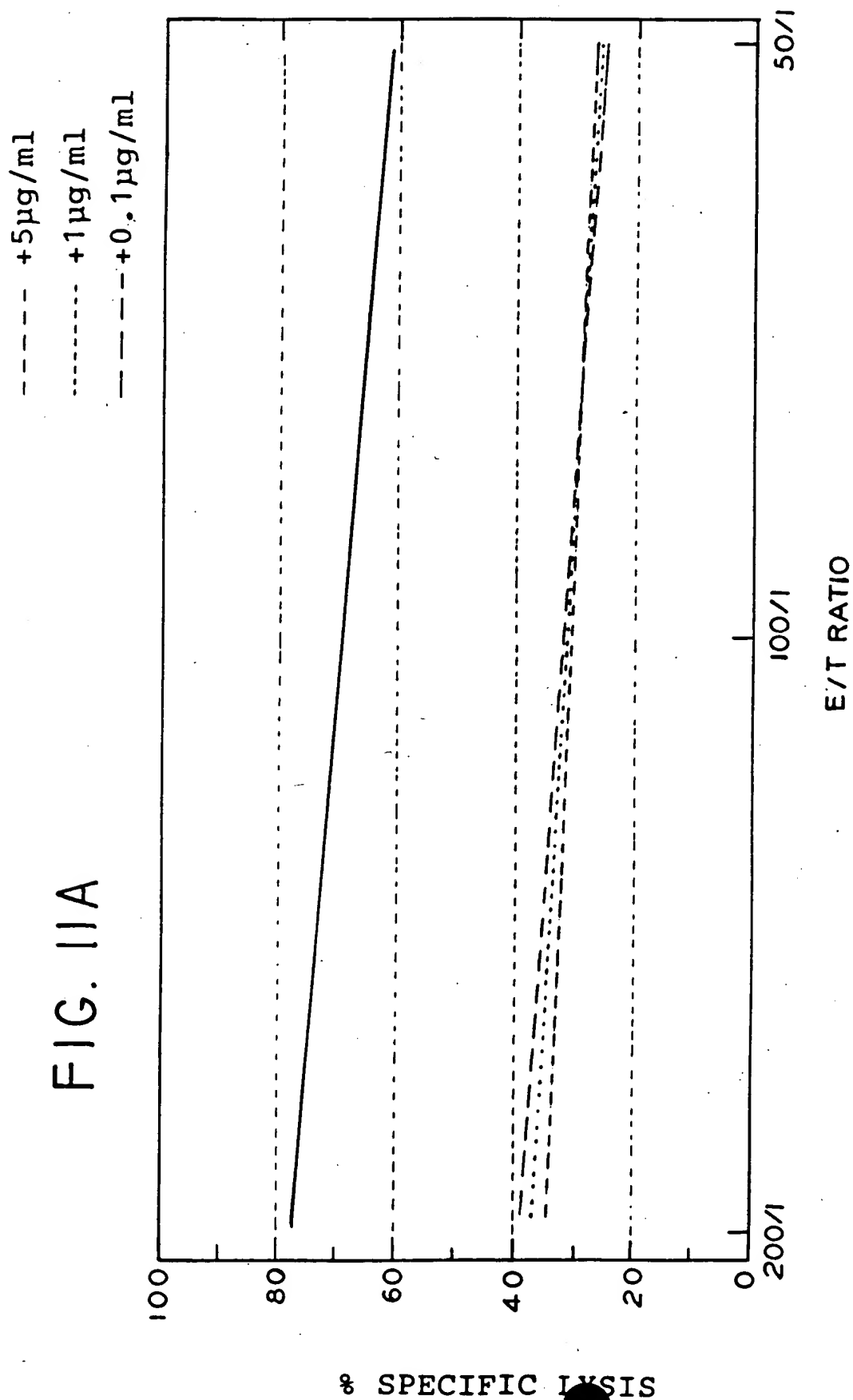


FIG. IIA

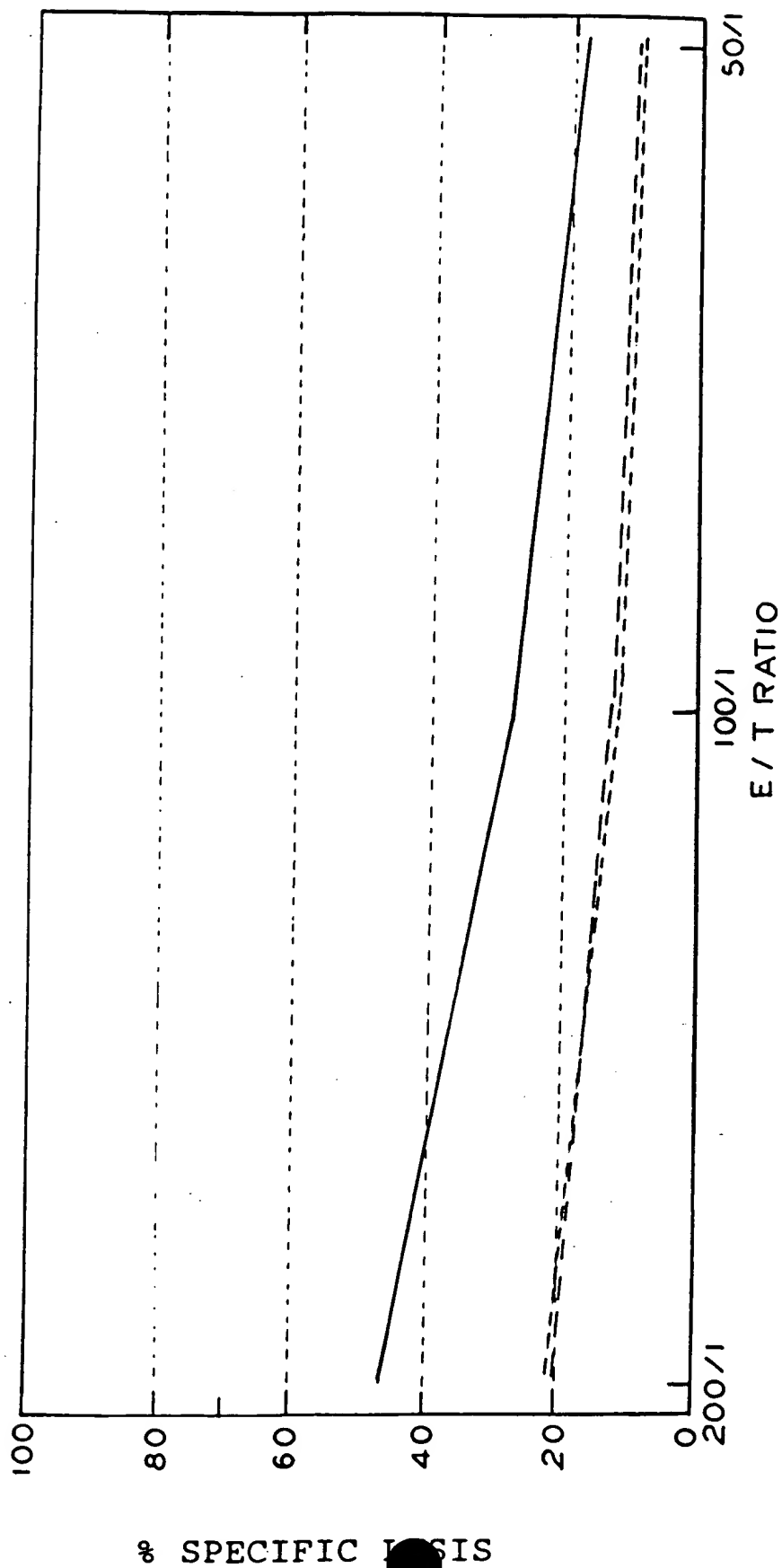


% SPECIFIC LYSIS

14 / 53

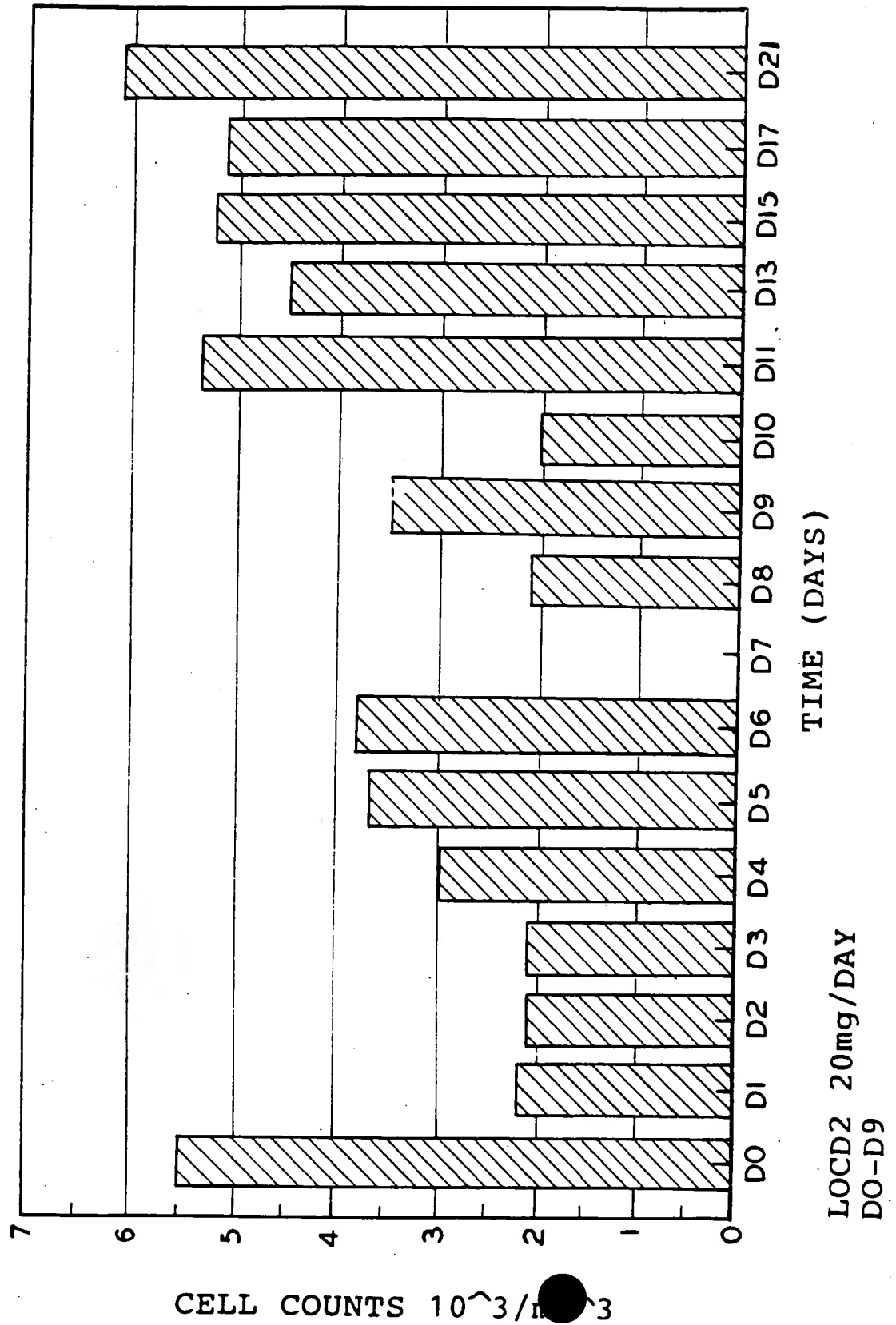
----- + 5 μ g/ml
 - - - - - + 1 μ g/ml
 ----- + 0.1 μ g/ml

FIG. IIB



% SPECIFIC LYSIS

FIG. 12



CELL COUNTS $10^3/\text{mm}^3$

TIME (DAYS)

CD2(LEU5b) CD4(LEU3a) CD8(LEU2a) CD8 CD11b+ IgM+

Time (Days)	CD2(LEU5b)	CD4(LEU3a)	CD8(LEU2a)	CD8 CD11b+	IgM+
D0	4200	3500	2000	1500	1000
D1	1000	1200	1000	800	500
D2	1000	1200	1000	800	500
D3	1000	1200	1000	800	500
D4	1000	1200	1000	800	500
D5	1000	1200	1000	800	500
D6	1000	1200	1000	800	500
D7	1000	1200	1000	800	500
D8	1000	1200	1000	800	500
D9	1000	1200	1000	800	500
D10	1000	1200	1000	800	500
D11	1000	1200	1000	800	500
D12	1000	1200	1000	800	500
D13	1000	1200	1000	800	500
D14	1000	1200	1000	800	500
D15	1000	1200	1000	800	500
D16	1000	1200	1000	800	500
D17	1000	1200	1000	800	500
D18	1000	1200	1000	800	500
D19	1000	1200	1000	800	500
D20	1000	1200	1000	800	500
D21	1000	1200	1000	800	500

lgM+: B CELLS
CD8+CD11b+: NK CELLS

17 / 53

FIG. 14

MONKEY #19 (@ AFTER LOCD2 10 DAYS

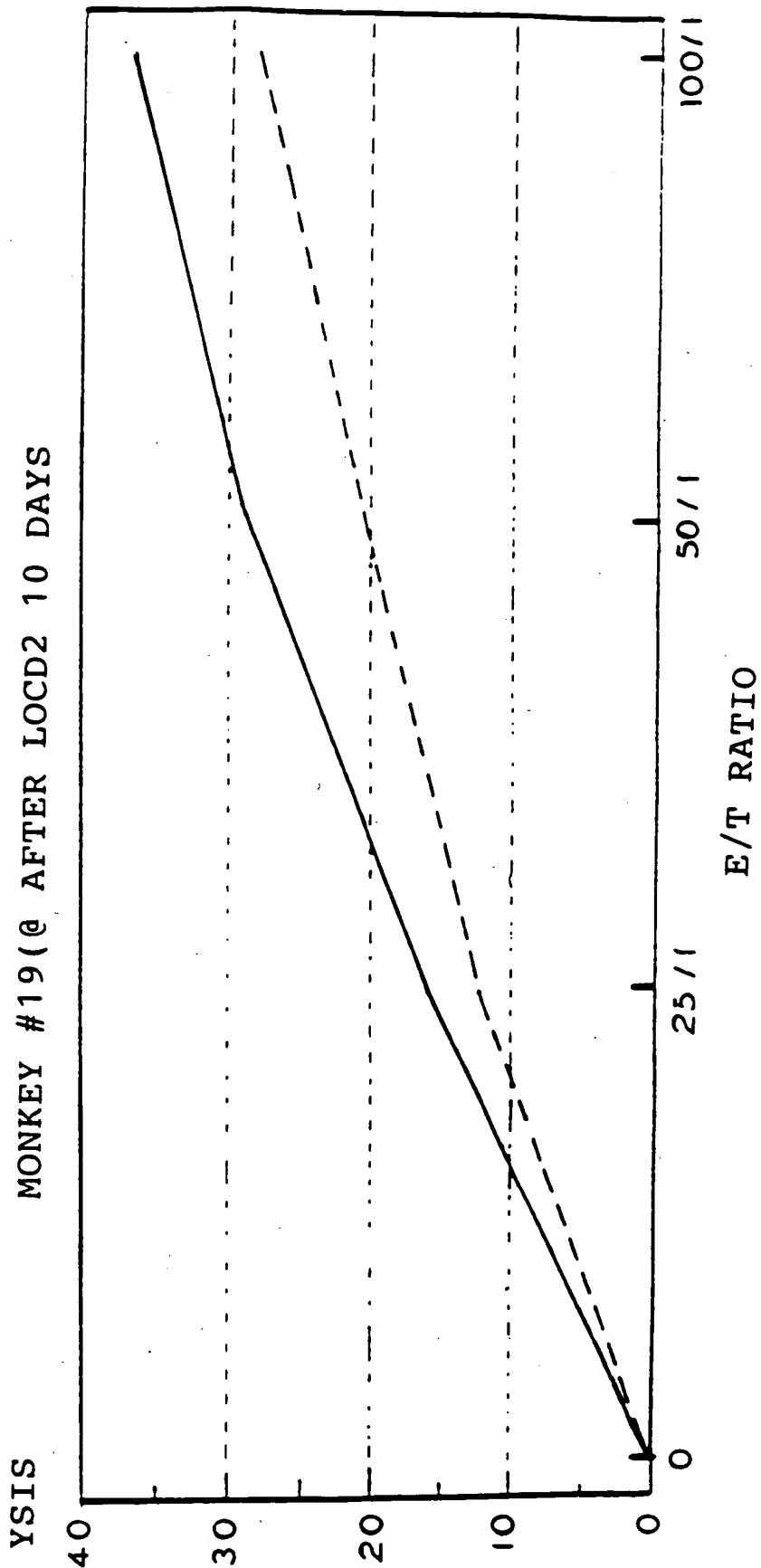
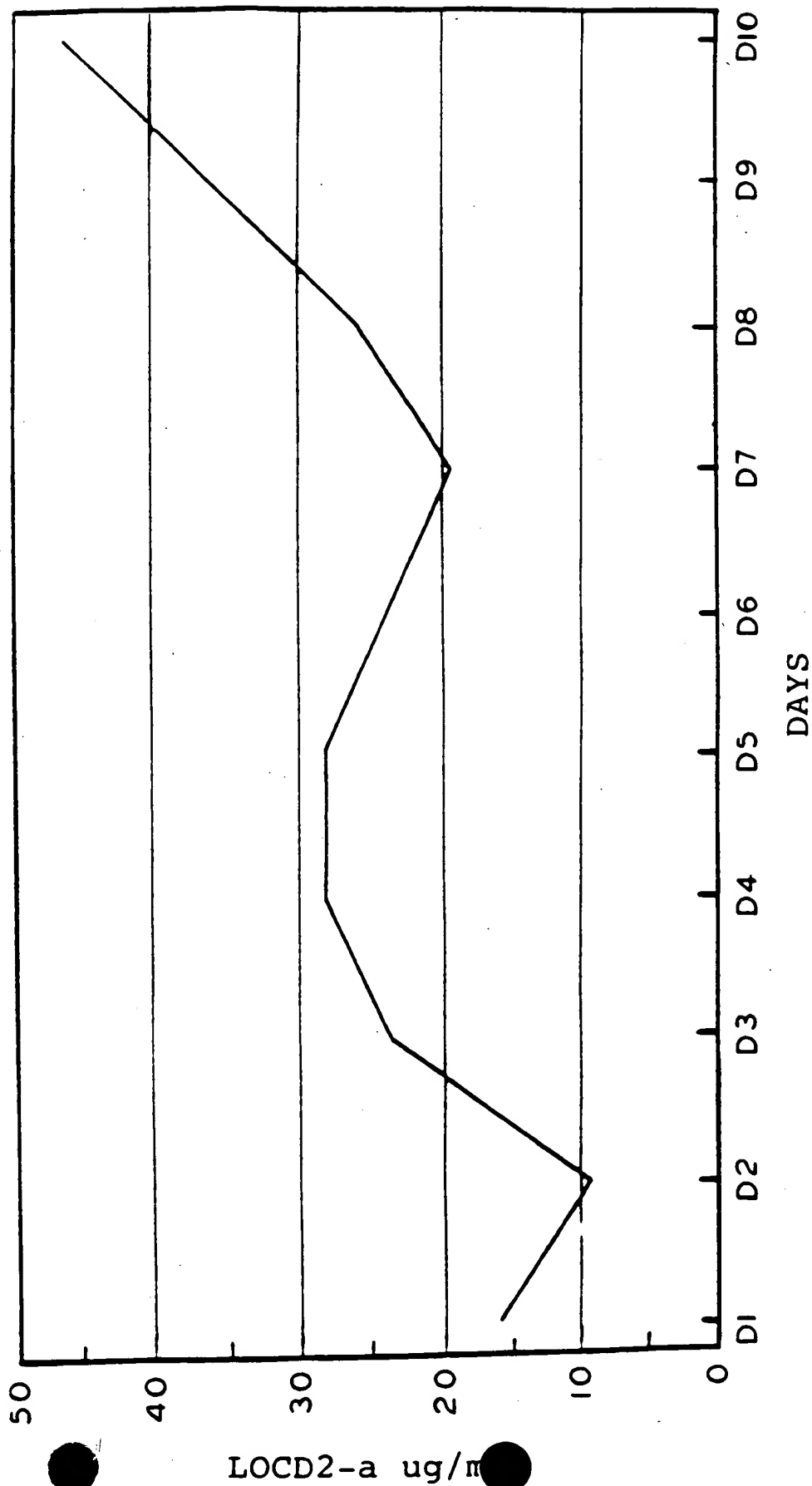


FIG. 15

CYNOMOLGUS MONKEY 1992



20/53

FIG. 17A

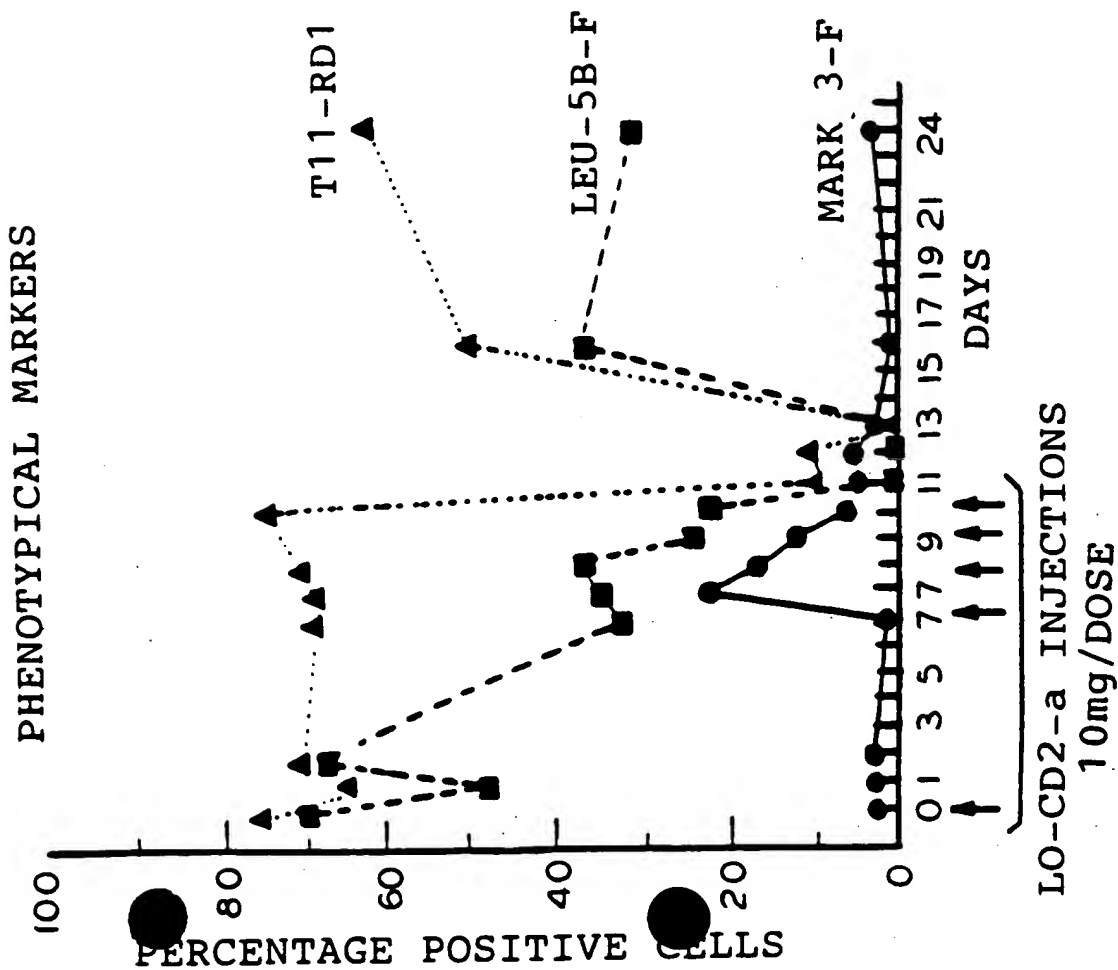


FIG. 17B

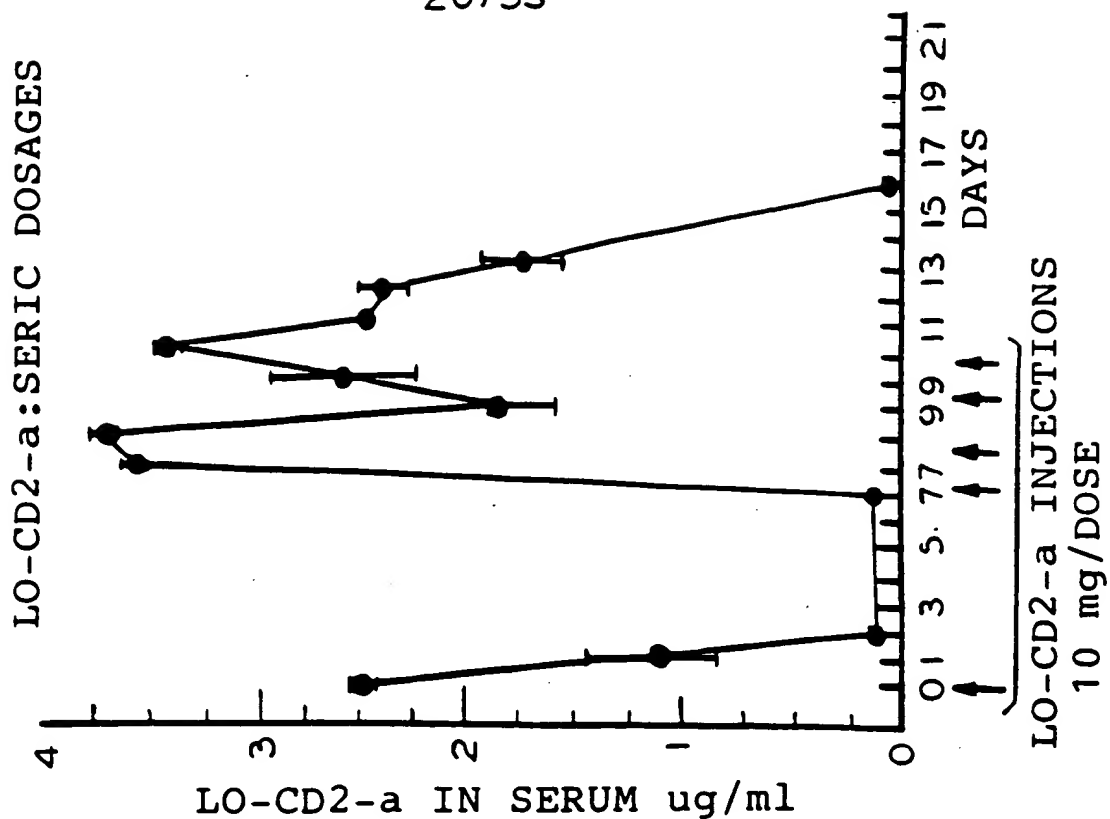


FIG. 18A

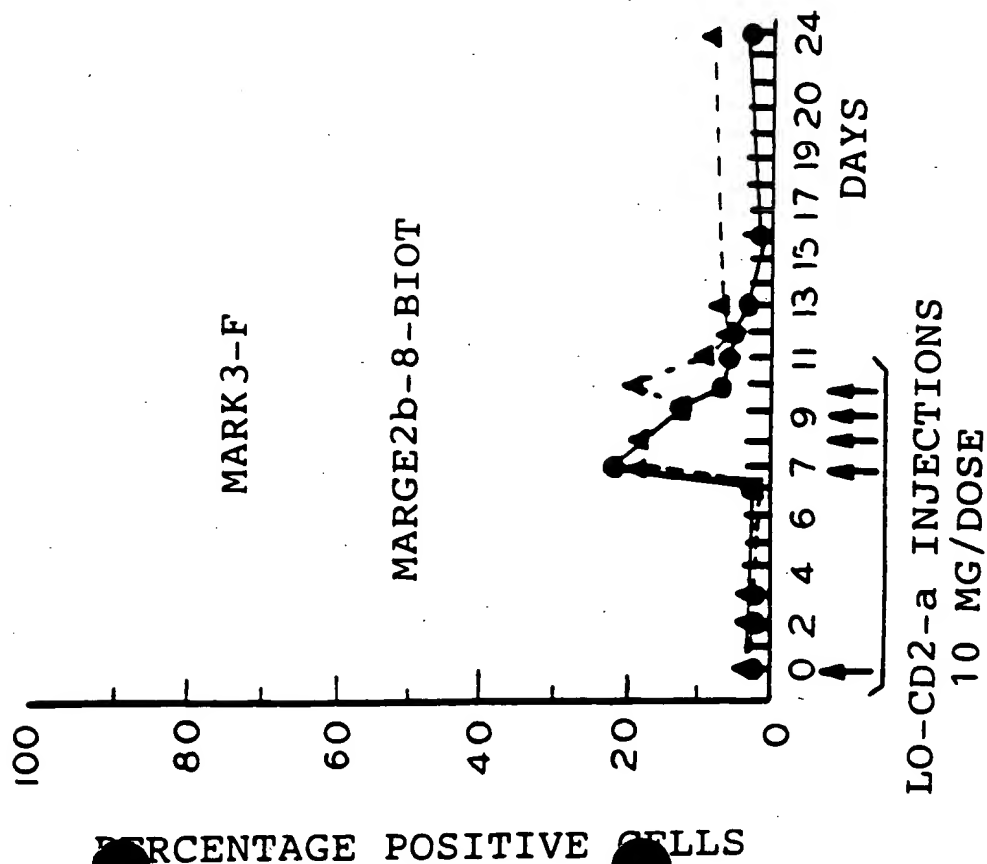
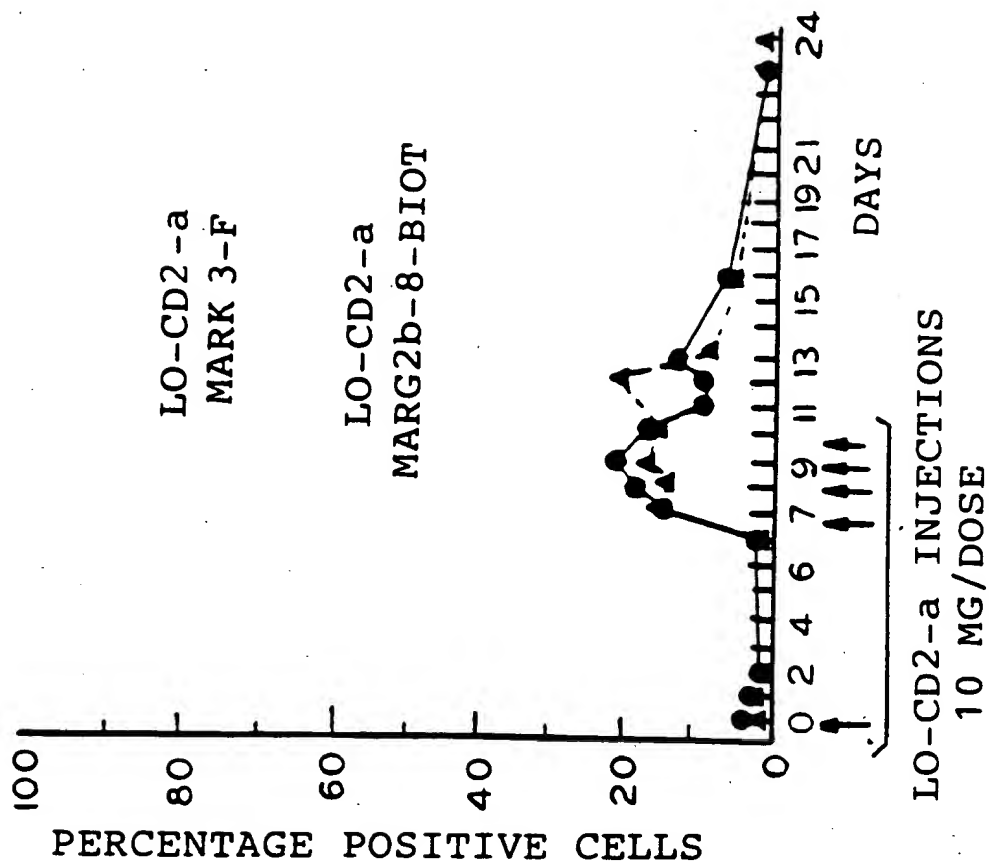
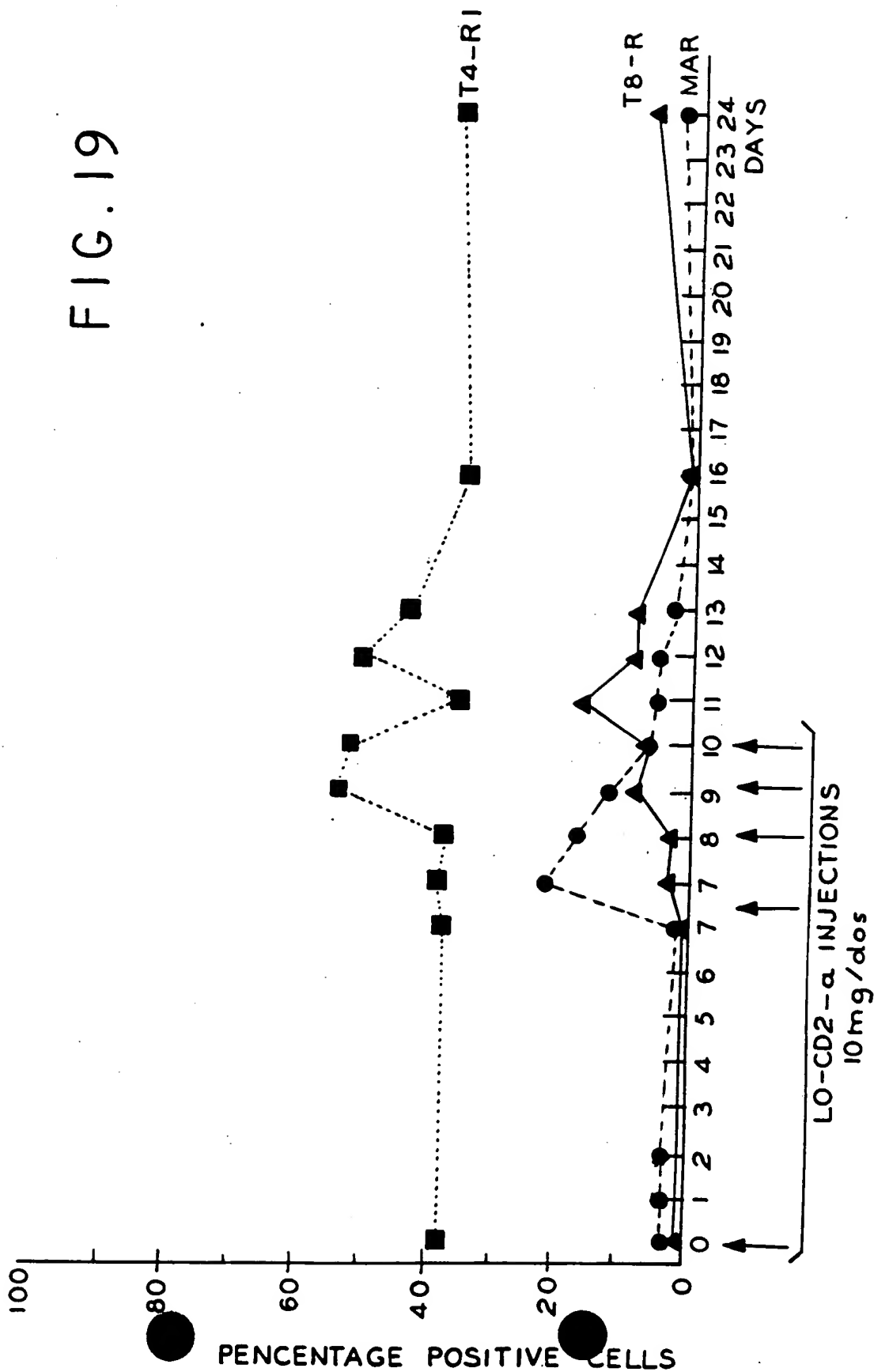


FIG. 18B



22 / 53

FIG. 19



862040" 22095060

23 / 53

FIG. 20

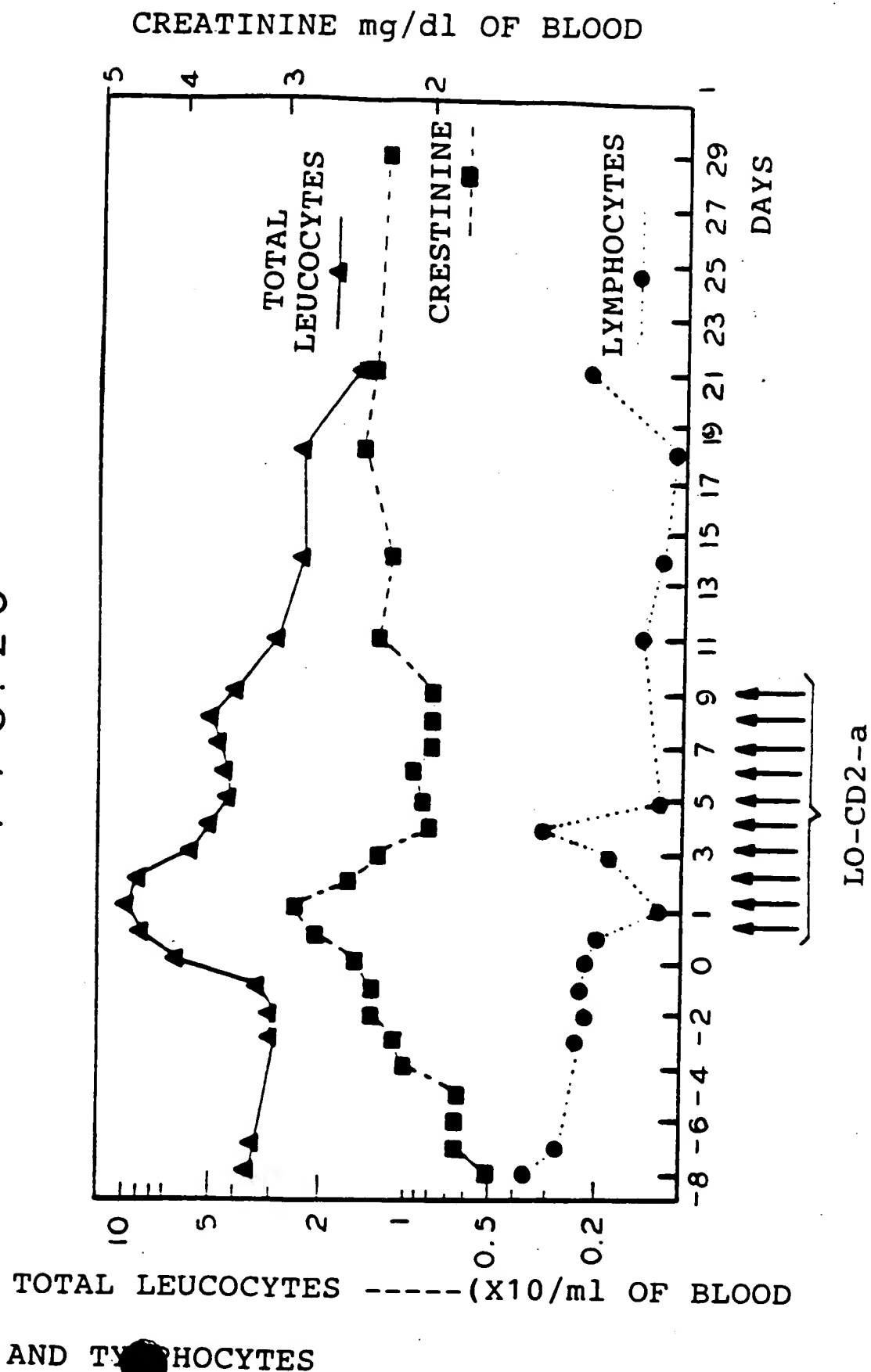


FIG. 21

LO-CD2-a: ug/ml OF SER

Legend:
B=BEFORE INJECTION
A=AFTER INJECTION

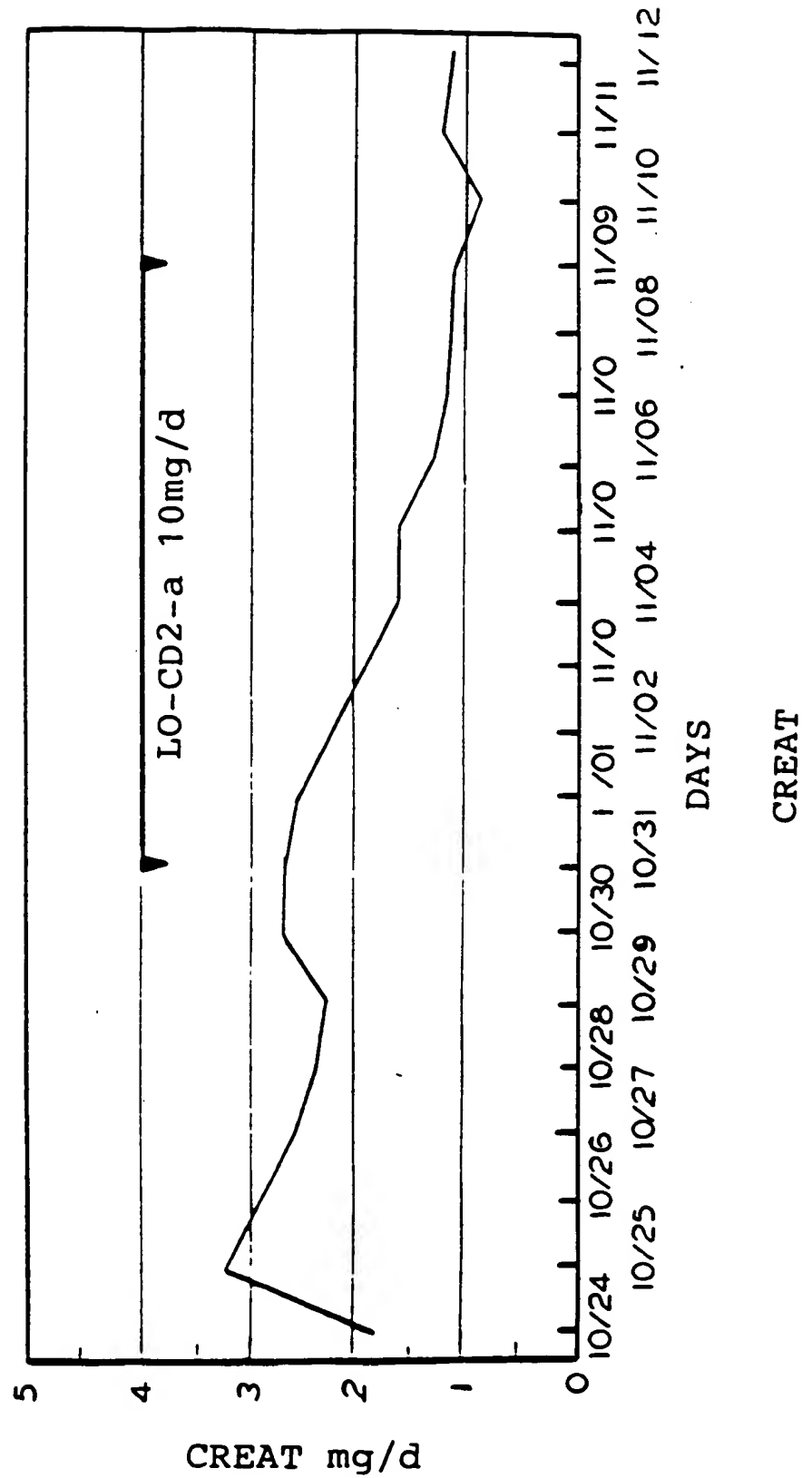
LO-CD2-a INJECTIONS
10mg/dose

Time (hours): 0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22

Concentration (ug/ml): 0 0.5 1 1.5 2 2.5 3 3.5 4 5

B=BEFORE INJECTION
A=AFTER INJECTION

FIG. 22



862040" 22095060

26 / 53

FIG. 23

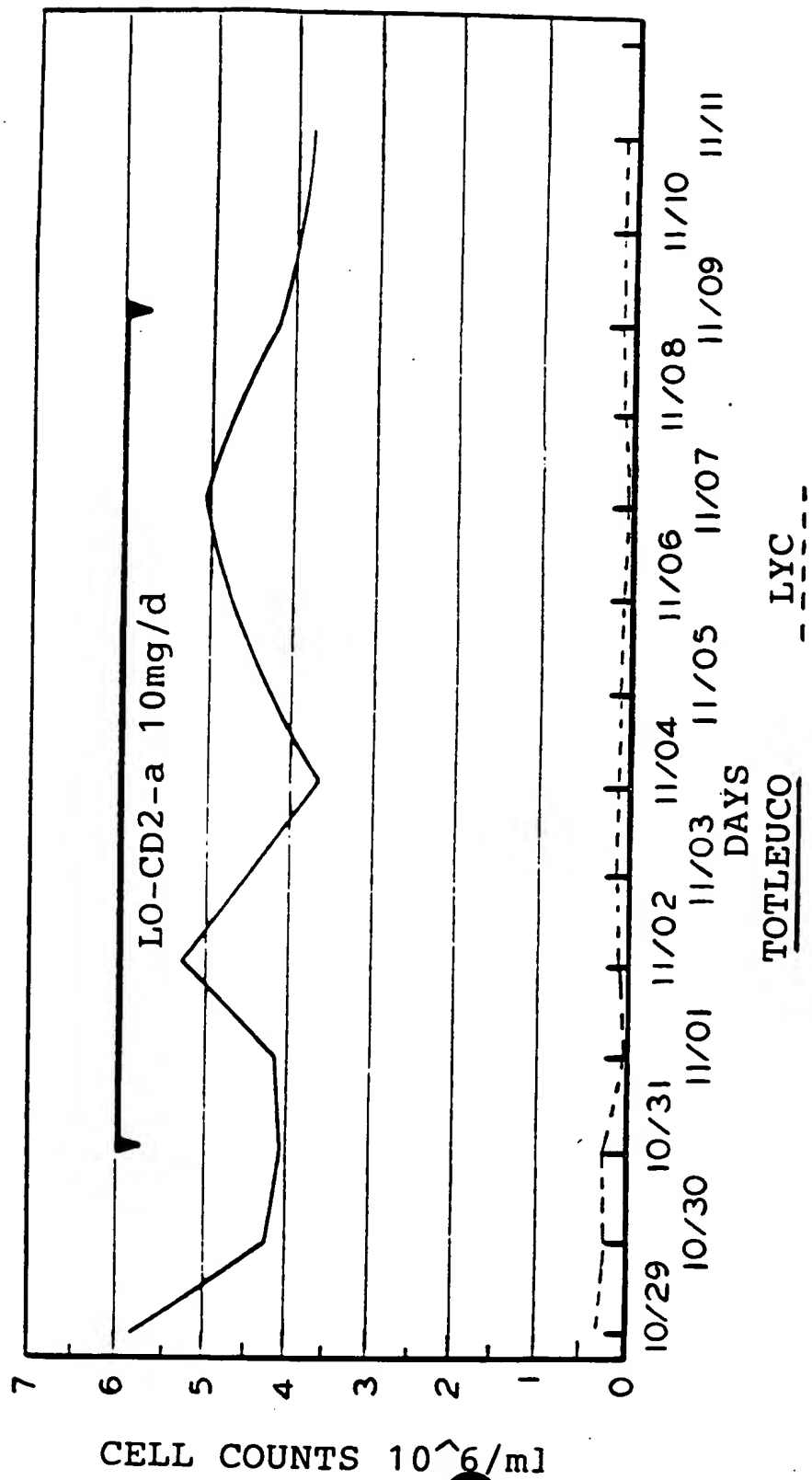
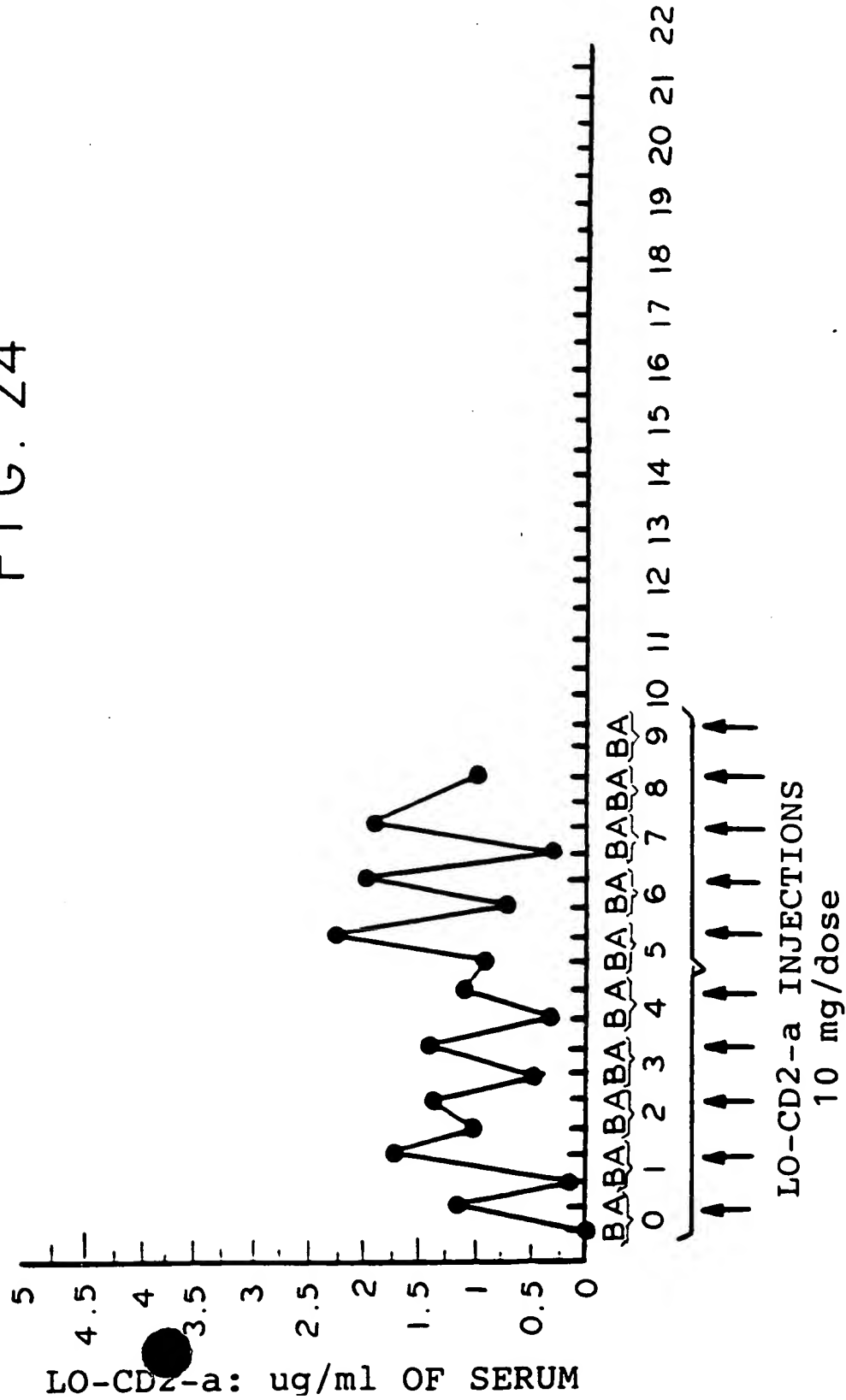
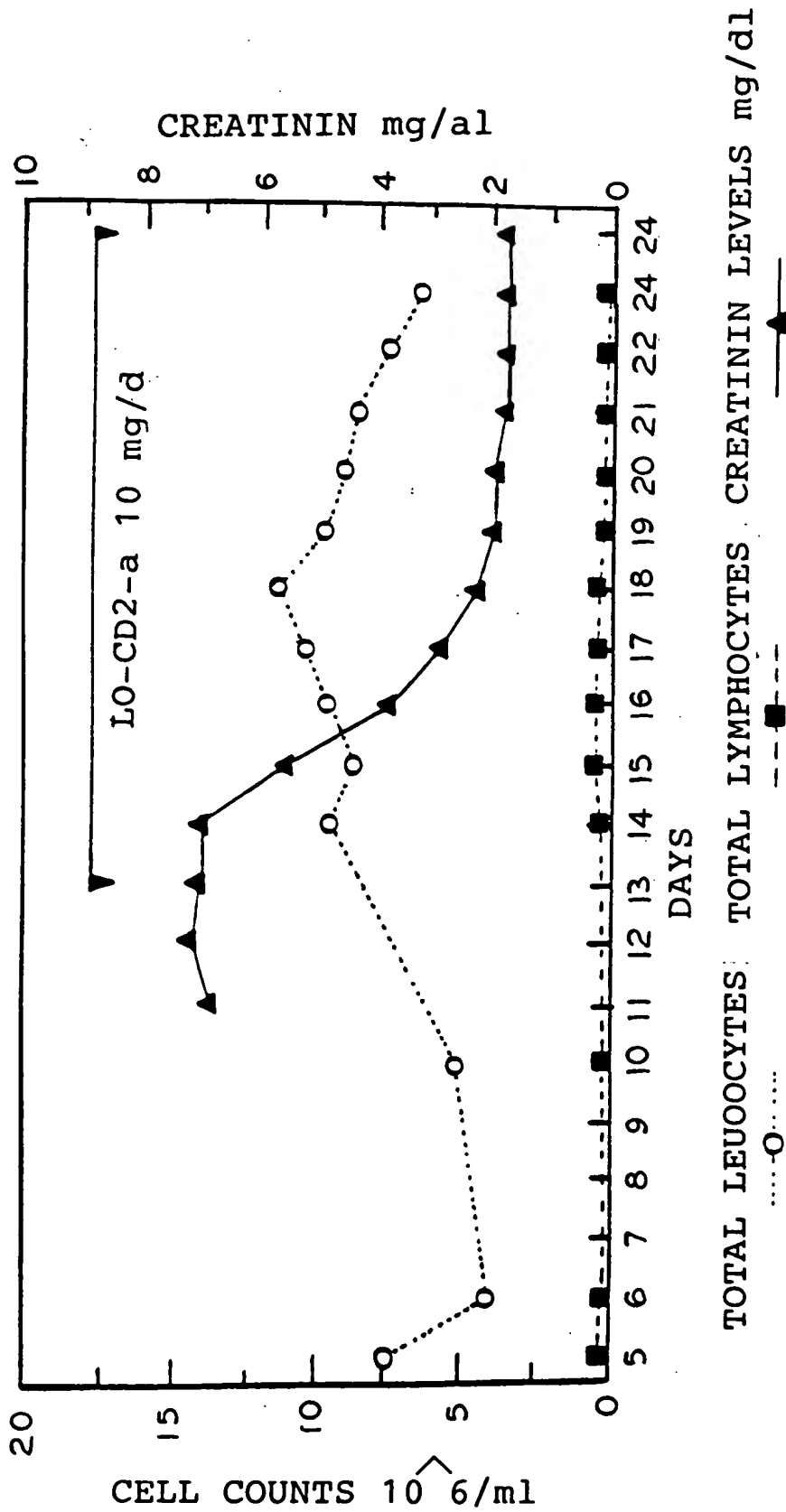


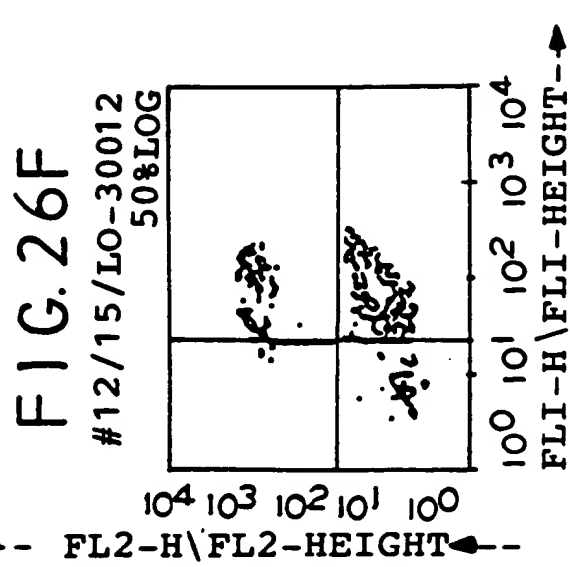
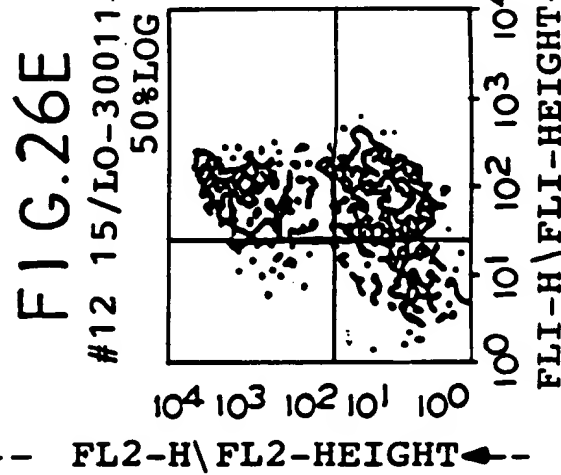
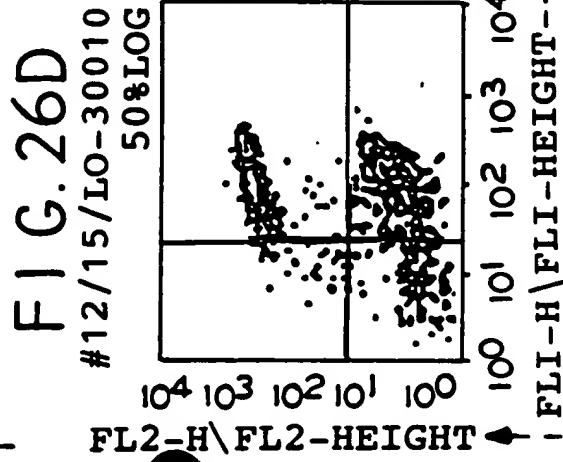
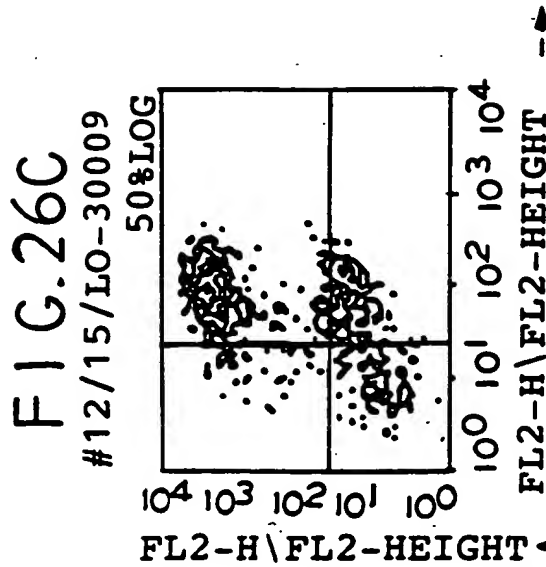
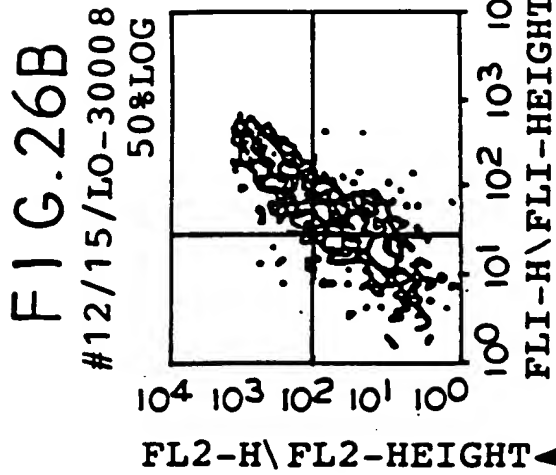
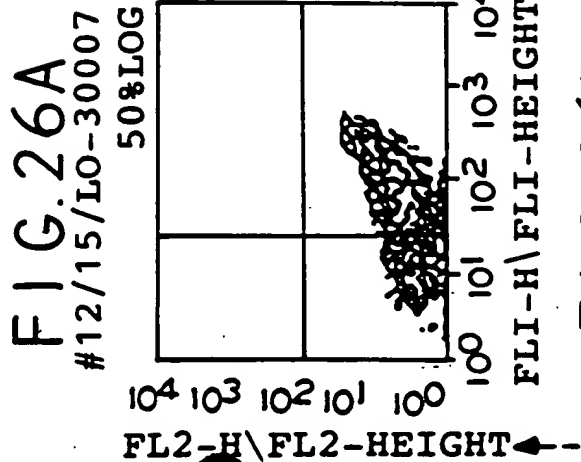
FIG. 24



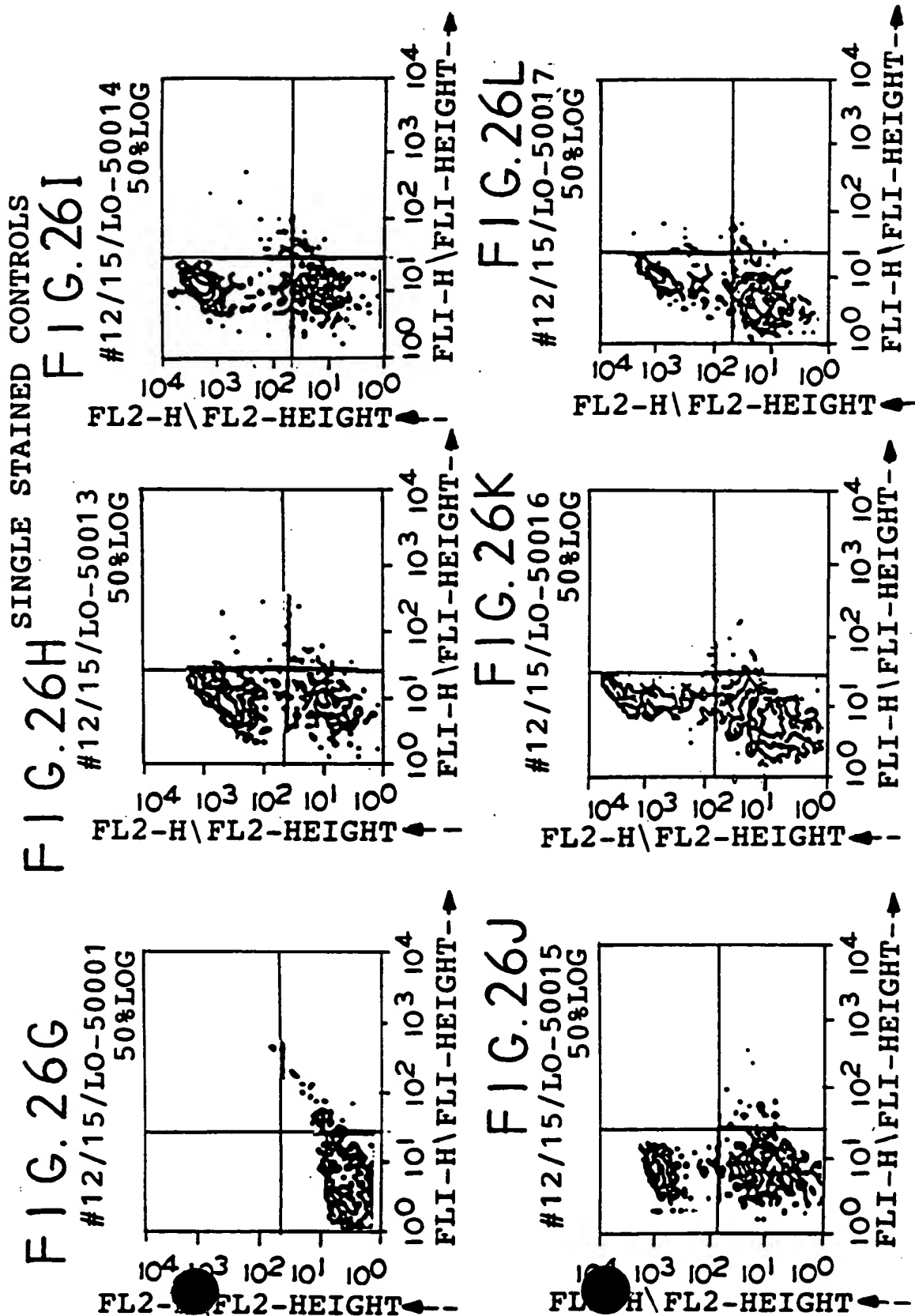
28/53

FIG. 25





SINGLE STAINED CONTROLS



31 / 53

FIG. 27A

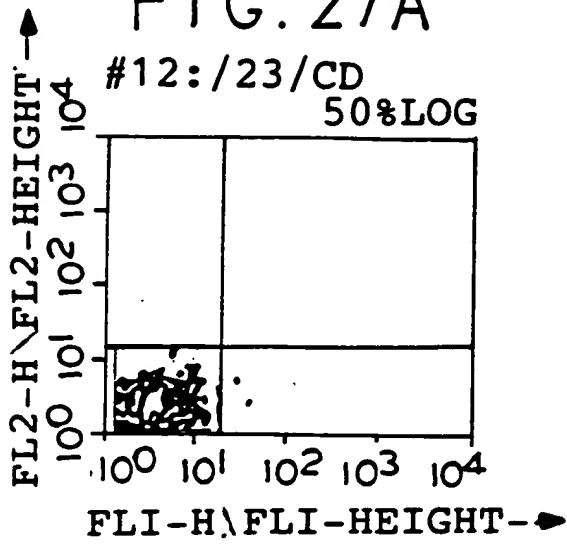


FIG. 27B

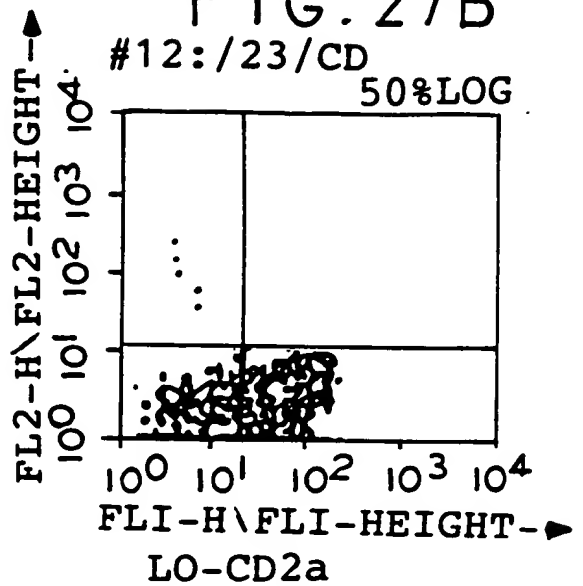


FIG. 27C

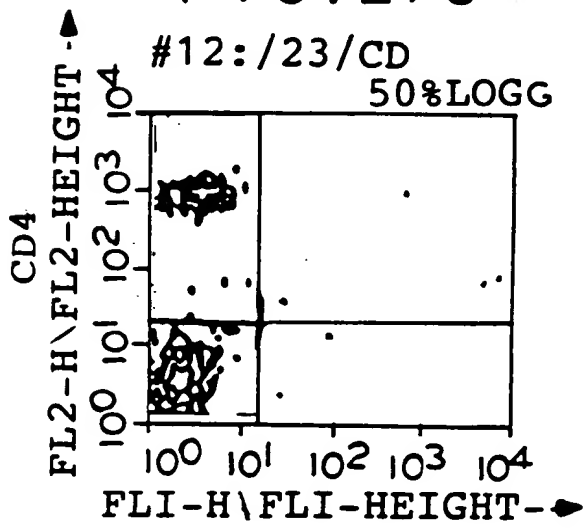


FIG. 27D

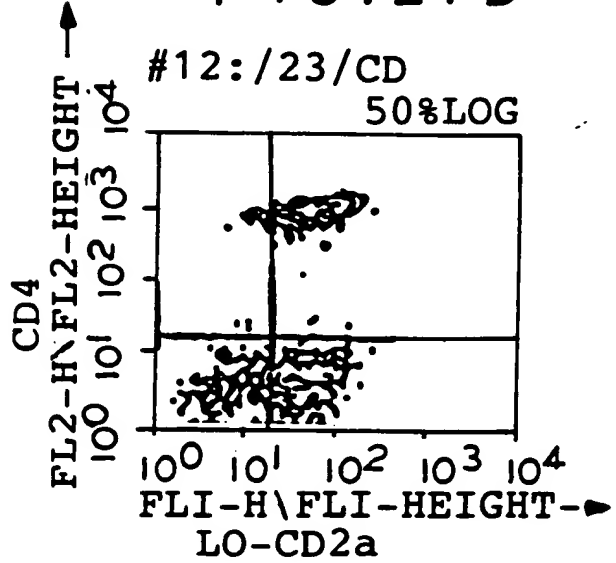


FIG. 27E

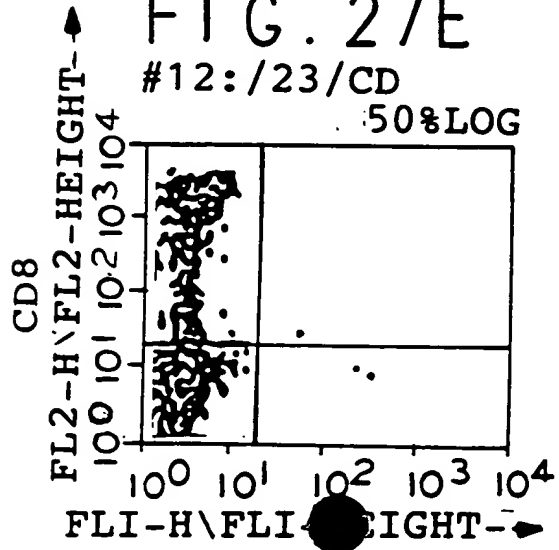
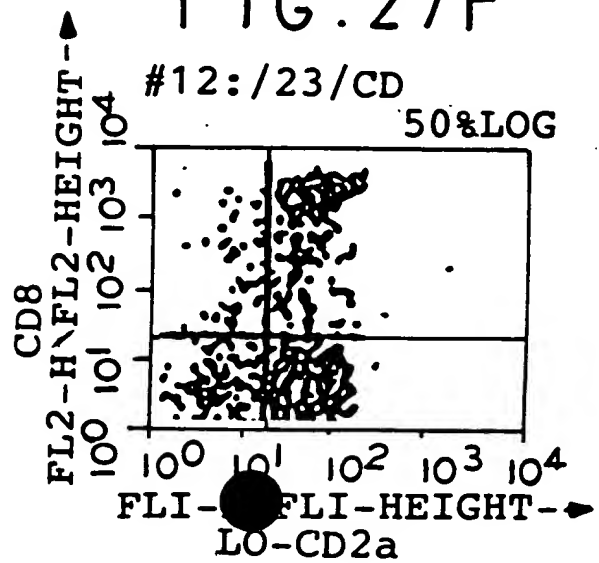


FIG. 27F



867040" 27095060

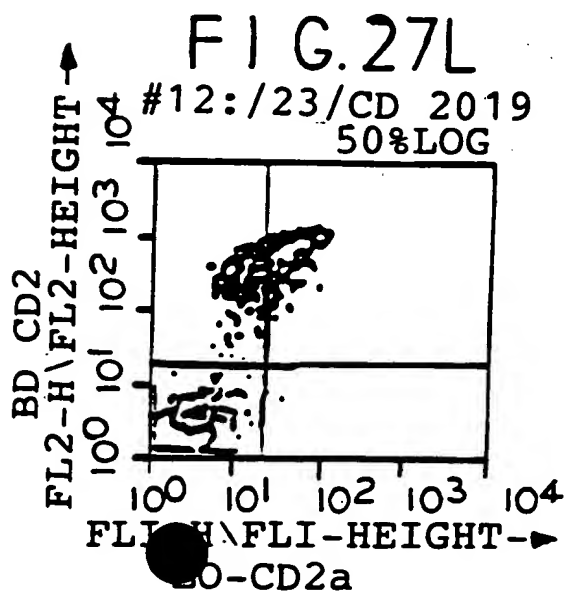
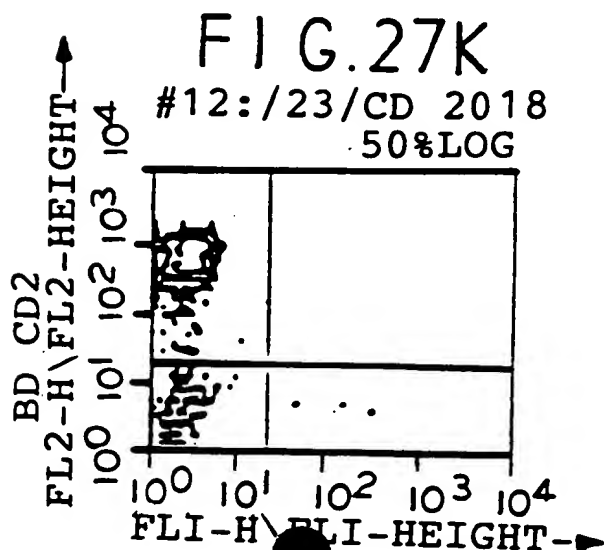
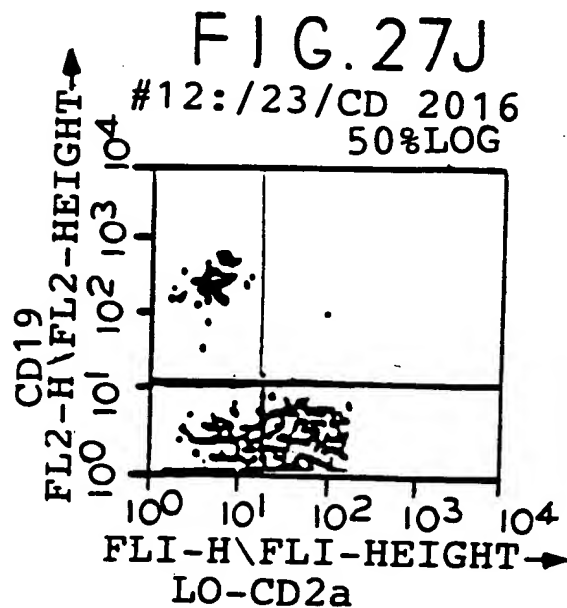
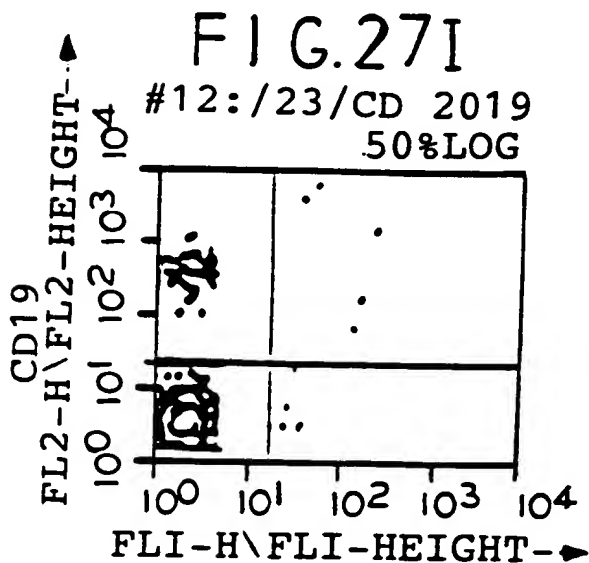
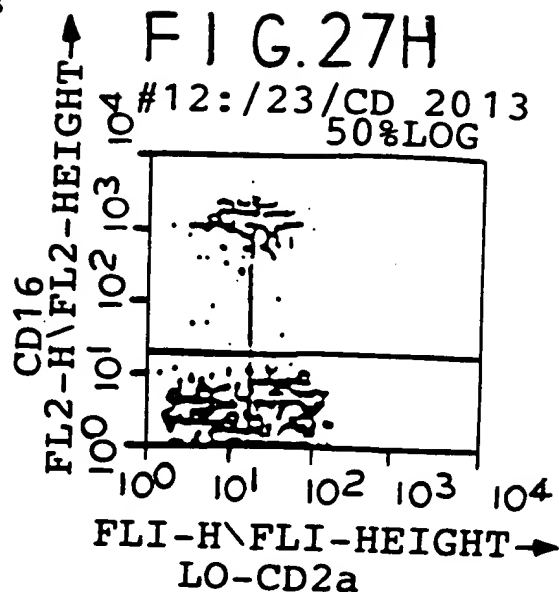
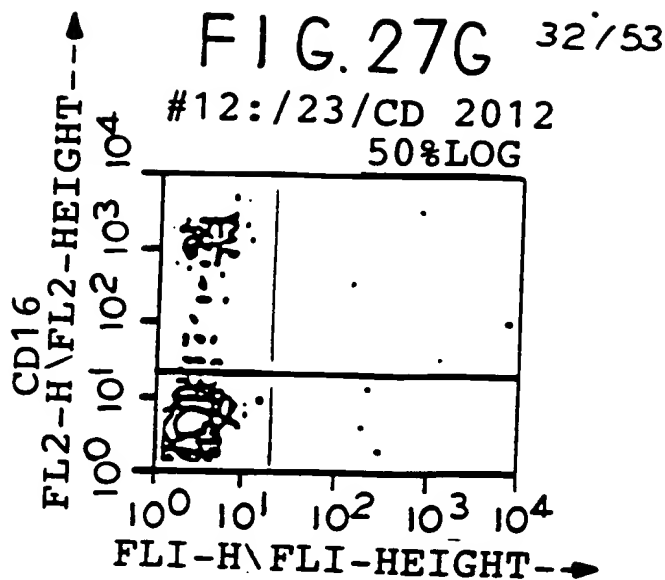


FIG. 28A

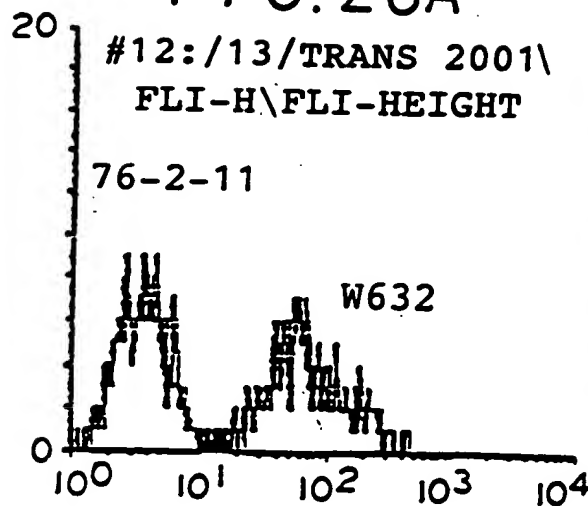


FIG. 28B

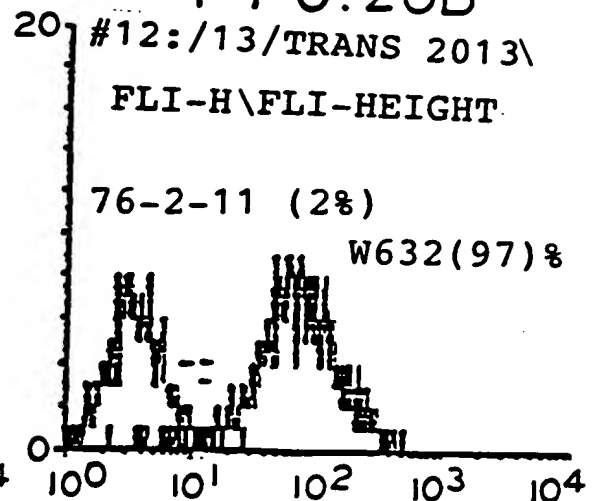


FIG. 28C

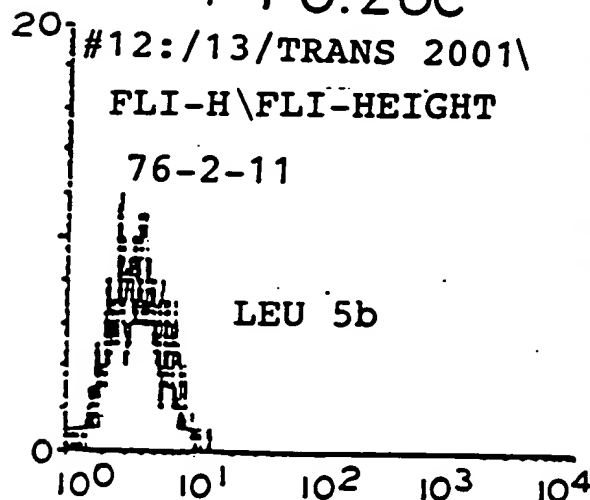


FIG. 28D

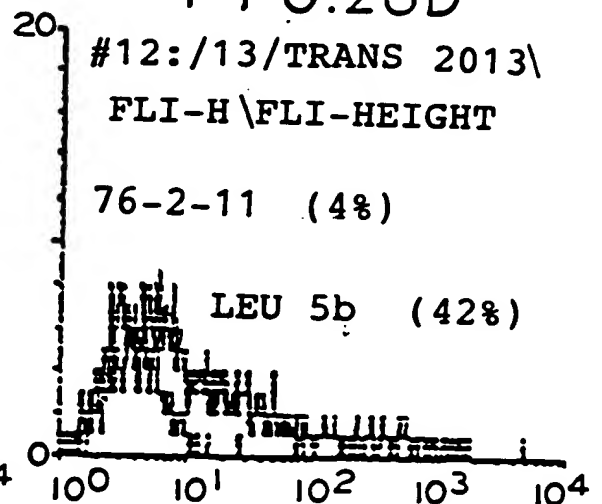


FIG. 28E

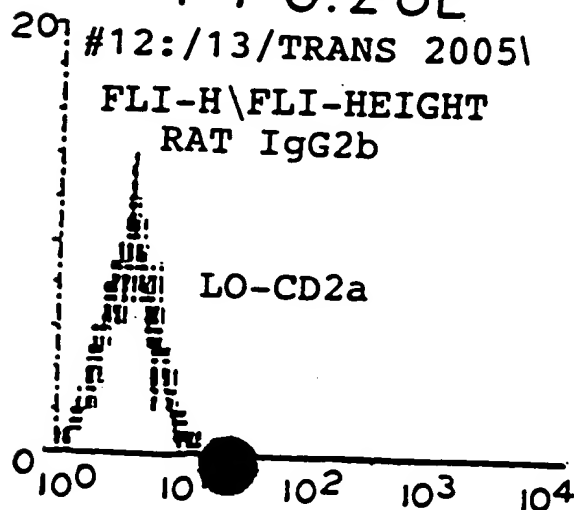
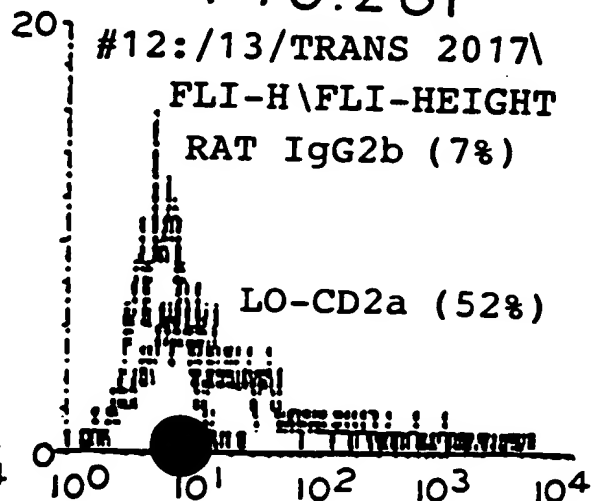


FIG. 28F



	10	20	30	
*	*	*	*	*
ATGATGAGTCCTGTCCAGTCCCTGTTTCTGTTATT				
M M S P V Q S L F L L L				
	110	120	130	
*	*	*	*	*
GACTGCCCATGTTGGCTGTCCATGTGTGGTAAGGC				
	210	220	230	
*	*	*	*	*
ATAGGATTTGTGCTAAGAGGATTCTAATGTAGATG				
	310	320	330	
*	*	*	*	*
TTAAAAATCACAAAACACACCGGGATCTCACAGGA				
	410	420	430	
*	*	*	*	*
TATTATAATTTTCAGGAACCAATGGTGATGTTGTGC				
		T N G D V V		
	510	520	530	
*	*	*	*	*
AGTCAGAGTCTCTTACATAGTAGTGGAACACCTA				
S Q S L L H S S G N T Y				
	610	620	630	
*	*	*	*	*
TGGAATCTGGGGTCCCCAACAGGTTTCAGTGGCAGT				
L E S G V P N R F S G S				
	710	720	730	
*	*	*	*	*
CTGCATGCAATTTACCCATTATCCGTATACGTTTG				
C M Q F T H Y P Y T F				

MATCH WITH FIG. 29B

09056072-040798

FIG. 29B

40 50 60 70
 * * * * *
 GCTTTGGATTCTGGGTAAGTAGAGAATGAGTTACA
 L W I L G

140 150 160 170
 * * * * *
 AGGTCCTATTTTCTAAGATGGACACTTGAGATTCC

240 250 260 270
 * * * * *
 AGAAGGTGTATGCCATTTAGGATCTGCAACCGAAT

340 350 360 370
 * * * * *
 AATGAGTAACAAAAAGTAATTCACAAAGATTGGTT

440 450 460 470
 * * * * *
 TGACCCAGACTCCACCTACTTTATTGGCTACCATT
 L T Q T P P T L L A T I

540 550 560 570
 * * * * *
 TTTAAATTGGTTGCTACAGAGGACAGGCCAATCTC
 L N W L L Q R T G Q S

640 650 660 670
 * * * * *
 GGGTCAGGAACAGATTTCACTCAAATCAGTGG
 G S G T D F T L K I S G

740 750 760
 * * * * *
 GAGCTGGGACCAAGCTGGAAGTGA
 G A G T K L E L K>

MATCH WITH FIG. 29A

MATCH WITH FIG. 29C

0095060220404686

FIG. 29C

80 90 100
 * * * * *
 GGACAAGAATGGGGATGGAGGATGAGTTCT

180 190 200
 * * * * *
 ATTACTTGATAATGAGAAATTACAGATGAG

280 290 300
 * * * * *
 TGT TTTGTGAAAAAGCATTTGGTATATTTT

380 390 400
 * * * * *
 GCAAATTTTGCACATAACTTTGTTCTGATC

480 490 500
 * * * * *
 GGACAATCAGTCTCCATCTCTTGCAGGTCA
 G Q S V S I S C R S>

580 590 600
 * * * * *
 CACAGCCGCTAATTTATTTGGTATCCAAAC
 P Q P L I Y L V S K>

680 690 700
 * * * * *
 AGTGGAAGTTGAGGATTTGGGGGTTATTA
 V E A E D L G V Y Y>

MATCH WITH FIG. 29B

09056072-040798

FIG. 30A

10 20 30 40
 * * * *
 ATGAAATGCAGGTGGATCATCTTCTTCTTGATGGCAGTAGCTACAG
 M K C R W I I L F L M A V A T

110 120 130 140
 * * * *
 CACTATCTTGGATTCTTGCAACAGGGTCAACTCAGAAAGTTCAG
 V N S E V Q

210 220 230 240
 * * * *
 TGCAAGGCTTCTGGCTATATATTTATAGAACTACTATATGTACTGGG
 C K A S G Y I F T E Y Y M Y W

310 320 330 340
 * * * *
 ACGGTAGTATTGATTATGTTGAGAAAGTTCAAAAGAGGCCACACT
 D G S I D Y V E K F K K K A T L

410 420 430 440
 * * * *
 TGAGGACACAGCAACCTATTTTGTGCTAGGGGAAATTCAACTAT
 E D T A T Y F C A R G K F N Y

Match with FIG. 30B

50 * 60 * 70 * 80 * 90 * 100 *
GTAAGGCACTCCCAAGTCCTAAACTTGAGAGATCATACACTGGGACACAGTGA
G> ()

150 * 160 * 170 * 180 * 190 * 200 *
 CTGCAGCAATCTGGGCTGAGCTTACAGAGACCGGGCCCTCAGTCAAGTTGTCG
 L Q Q Q S G P E L Q R P G A S V K L S>

250 * 260 * 270 * 280 * 290 * 300 *

TGAAGCAGAGGCCTAAACAGGCCCTGGAATTAGTAGGAAGGATCGATCCTGAAG

V K Q R P K Q G L E L V G R I D P E>

350 * 360 * 370 * 380 * 390 * 400 *

GACTGCAGATACATCGTCCAATACAGCCTACATGCAACTAGCAGCCTGACATC

T A D T S S N T A Y M Q L S S L T S >

CGATTGCTTACTGGGCCAAGGCACCCCTGTCACAGTCTCCTCA
R F A Y W G Q G T L V T V S S >

FIG. 31

	FR 1	*	*	20	CDR 1	30	40	FR 2	*
Rat Lo-CD2a Vk	DVVL	TQ	TPPT	LLATIGQSVS	ISCRSSQSL	L	HSSGNTYLNW	LLQRTGQSPQ	
Humanized Vk	---	M---	S---	--V-L--PA-	-----	-----	-----	-----P-----	
Human HUM5400 Vk	---	M---	S-LS	-PV-L--PA-	-	-V	Y-D---	H---FQ--P-----R	

	CDR 2	60	70	FR 3	80	90	CDR 3	100
Rat LO-CD2a Vk	PLIYLVSKLE	SGV	PNRFSGS	GS	GTDFTLKI	SGVEAEDLGV	YYCMQFTHYP	
Humanized Vk	-----	---	D---	-----	-----	-----V---	-----	
Human HUM5400 Vk	R---	K--NRD	----	D-----	-----	-R-----V--	-----G--W-	

39/53

	FR 4	110
Rat LO-CD2a Vk	YTFGAGTKLE	LK
Humanized Vk	-----Q-----	I-
Human HUM5400 Vk	-----Q-----	I-

40/53

FIG. 32A

10 20 30
* * * * *
AAGCTTCATGATGAGTCCTGTCCAGTCCTTGTTTC
M M S P V Q S L F

110 120 130
* * * * *
GAGTTCTGACTGCCCATGTTGGCTGTCCATGTGTG

210 220 230
* * * * *
AGATGAGATAGGATTTGTGCTAAGAGGATTCTAAT

310 320 330
* * * * *
ATATTTTTTTAAAAATCACAAAACACACCGGGATCT

410 420 430
* * * * *
TCTGATCTATTATAATTCAGGAACCAATGGTGAT
T N G D

510 520 530
* * * * *
CAGGTCAAGTCAGAGTCTCTTACATAGTAGTGGA
R S S Q S L L H S S G

610 620 630
* * * * *
TCCAAACTGGAATCTGGGGTCCCCGACAGGTTTCAG
S K L E S G V P D R F S

710 720 730
* * * * *
TTTATTACTGCATGCAATTTACCCATTATCCGTAC
V Y Y C M Q F T H Y P Y
TGGATCC

MATCH WITH FIG. 32B

09056072-040798

41/53

FIG. 32B

40 50 60 70
 * * * * *
 TGTATTGCTTTGGATTCTGGGTAAGTAGAGAATG
 L L L L W I L G>

140 150 160 170
 * * * * *
 GTAAGGCAGGTCCTATTTTCTAAGATGGACACTTG

240 250 260 270
 * * * * *
 GTAGATGAGAAGGTGTATGCCATTTAGGATTTGCA

340 350 360 370
 * * * * *
 CACAGGAAATGAGTAACAAAAAGTAATTCACAAAG

440 450 460 470
 * * * * *
 GTTGTGATGACCCAGAGTCCACCTTCATTATTGGT
 V V M T Q S P P S L L V

540 550 560 570
 * * * * *
 ACACCTATTTAAATTGGTTGCTACAGAGGCCAGGC
 N T Y L N W L L Q R P G

640 650 660 670
 * * * * *
 TGGCTCAGGGAGTGGAACAGATTTACACTCAAAA
 G S G S G T D F T L K

740 750 760 770
 * * * * *
 ACGTTGGACAAGGAACCAAGCTCAAAATCAAACG
 T G Q G T K L E I K>

MATCH WITH FIG. 32A

MATCH WITH FIG. 32C

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MATCH WITH FIG. 32B

42/53

FIG. 32C

80 90 100
* * * * *
AGTTACAGGACAAGAATGGG GATGGAGGAT

180 190 200
* * * * *
AGATTCCATTACTTGATAATGAGAAATTAC

280 290 300
* * * * *
ACCAATTGTTTGTGAAAAAGCATTTGGT

380 390 400
* * * * *
ATTGGTTGCAAATTTTGCACATAACTTTGT

480 490 500
* * * * *
AACCTTGGGACAACCAGCTTCCATCTCTTG
T L G Q P A S I S C>

580 590 600
* * * * *
CAATCTCCACAGCCGCTAATTTATTTGGTA
Q S P Q P L I Y L V>

680 690 700
* * * * *
TCAGTGGAGTGGAAGCTGAGGATGTGGGGG
I S G V E A E D V G>

780 790 800
* * * * *
TGAGTAGAATTTAAACTTCTTCCTCAGT

FIG. 34A

10 20 30
 * * * * * * *
 AAGCTTCATGAAATGCAGGTGGATCATCCTCTTCT
 M K C R W I I L F

110 120 130
 * * * * * * *
 ACAGTGACACTATCTTTGGATTTCTTTCAACAGGG

210 220 230
 * * * * * * *
 GGTCTCCTGCAAGGCTTCTGGATACACCTTCACCG
 V S C K A S G Y T F T

310 320 330
 * * * * * * *
 CCTGAAGACGGTAGTATTGATTATGTTGAGAAGTT
 P E D G S I D Y V E K F

410 420 430
 * * * * * * *
 TGACCTCTGACGACACGGCCGTGTATTACTGTGCG
 L T S D D T A V Y Y C A

510 520 530
 * * * * * * *
 TGAGTCTTTACAACCTCTCTCTTCTATTTCAGCTTA

610 620 630
 * * * * * * *
 AGGGACACCTTGGGAGTCAGAAAGGGTCATTGGGA

MATCH WITH FIG. 34B

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FIG. 34B

40 50 60 70
 * * * * *
 TGATGGCAGTAGCTACAGGTAAGGCACTCCCAAGTC
 L M A V A T G>

140 150 160 170
 * * * * *
 GTCAACTCACAGGTGCAGCTGGTGCAGTCTGGGGCT
 V N S Q V Q L V Q S G A

240 250 260 270
 * * * * *
 AGTACTATATGTACTGGGTGCGACAGGCCCTGGAC
 E Y Y M Y W V R Q A P G

340 350 360 370
 * * * * *
 TAAGAAAAAGGTCACCCTGACCGCTGACACGTCCTC
 K K K V T L T A D T S S

440 450 460 470
 * * * * *
 AGAGGAAAGTTTAATTATAGTTTTGCTTACTGGGGC
 R G K F N Y R F A Y W G

540 550 560 570
 * * * * *
 AATAGATTTTACTGCATTTGTTGGGGGGGAAATGTG

640 650 660 670
 * * * * *
 GCCCGGGCTGATGCAGACAGACATGCTCAGCTCCCG

MATCH WITH FIG. 34A

MATCH WITH FIG. 34C

862040" 24095060

FIG. 34C

80 90 100
 * * * * *
 CTAAACTTGAGAGATCATA CACTTGGGAG

180 190 200
 * * * * *
 GAGGTGAAGAAGCCTGGGG CCTCAGTGAA
 E V K K P G A S V K>

280 290 300
 * * * * *
 AAGGGCTTGAGCTGATGGG AAGGATCGAT
 Q G L E L M G R I D>

380 390 400
 * * * * *
 TAGCACAGCCTACATGGAG CTGAGCAGCC
 S T A Y M E L S S>

480 490 500
 * * * * *
 CAAGGAACCCTGGTCACCG TCTCCTCAGG
 Q G T L V T V S S>

580 590 600
 * * * * *
 TGTATCTGAATTTTCAGGTC ATGAAGGACT

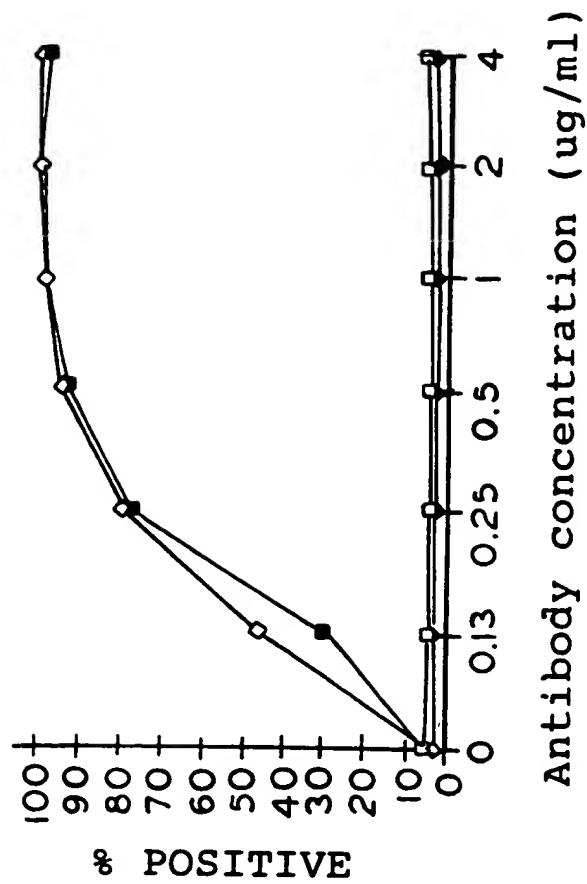
680 690 700
 * * * * *
 GACTTCATGGCCAGAGATT TATAGGGATC

MATCH WITH FIG. 34B

862040-22095060

FIG. 35

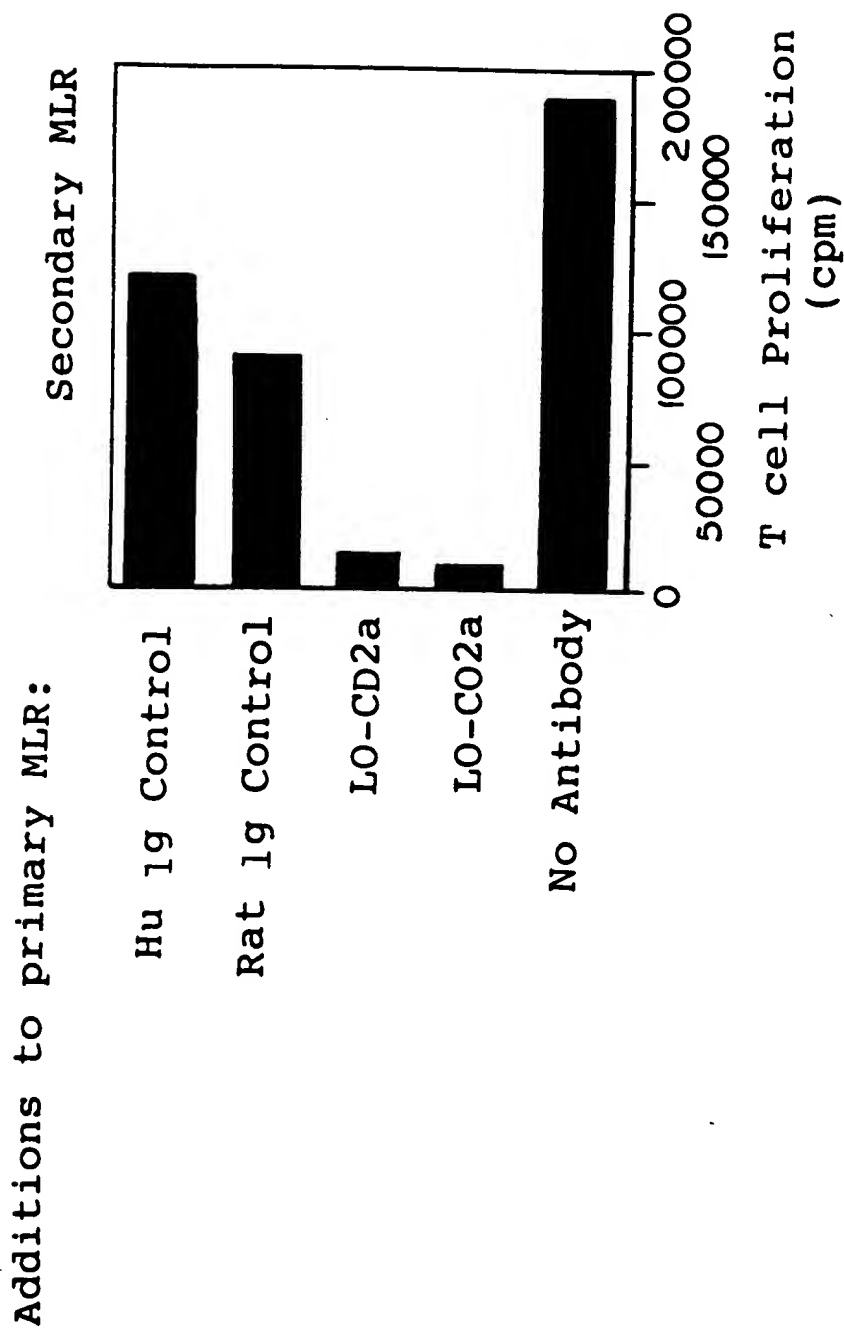
—●— LO-CD2a
 —○— Rat IgG2b control
 —◆— Human IgG control
 —◇— LO-CO2c Hu



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862040" 24095060

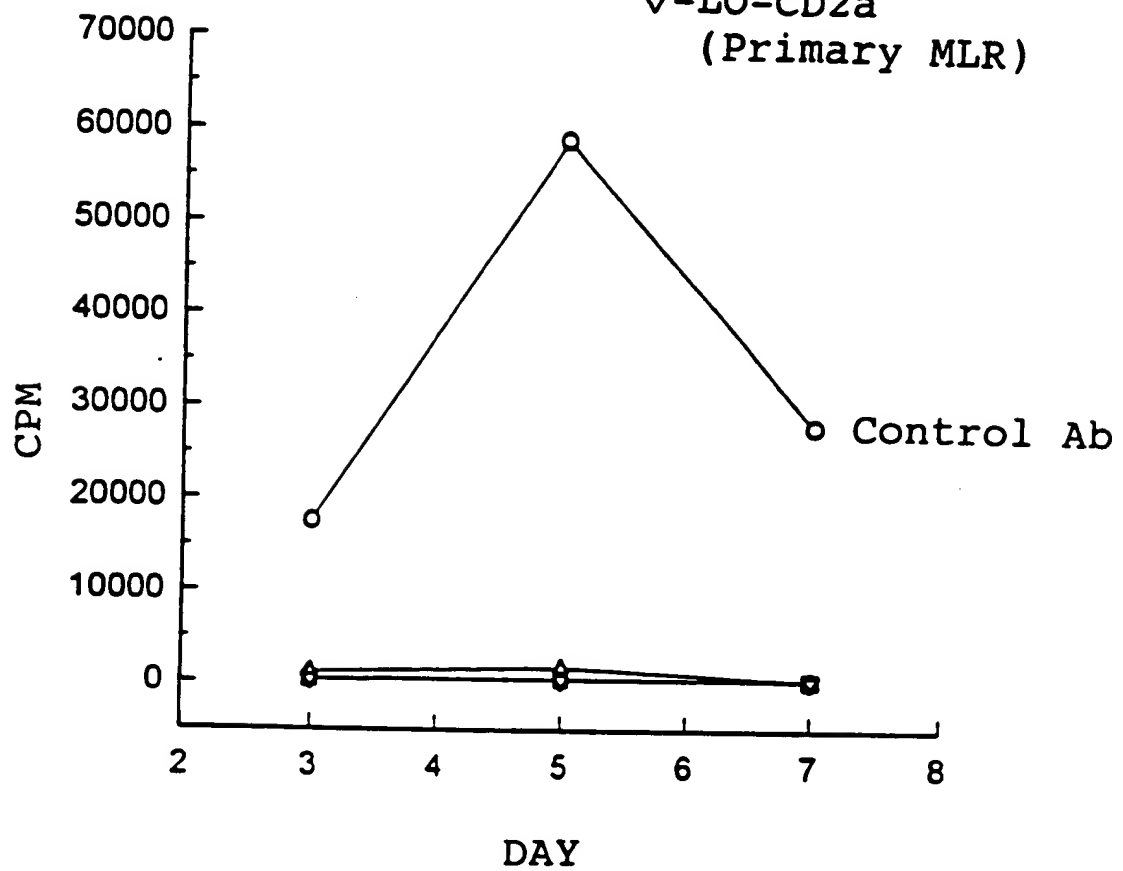
FIG. 36



49/53

FIG. 37

□ -LO-CD2a
△ -Control Ab
(Primary MLR)
▽ -LO-CD2a
(Primary MLR)



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FIG. 38A

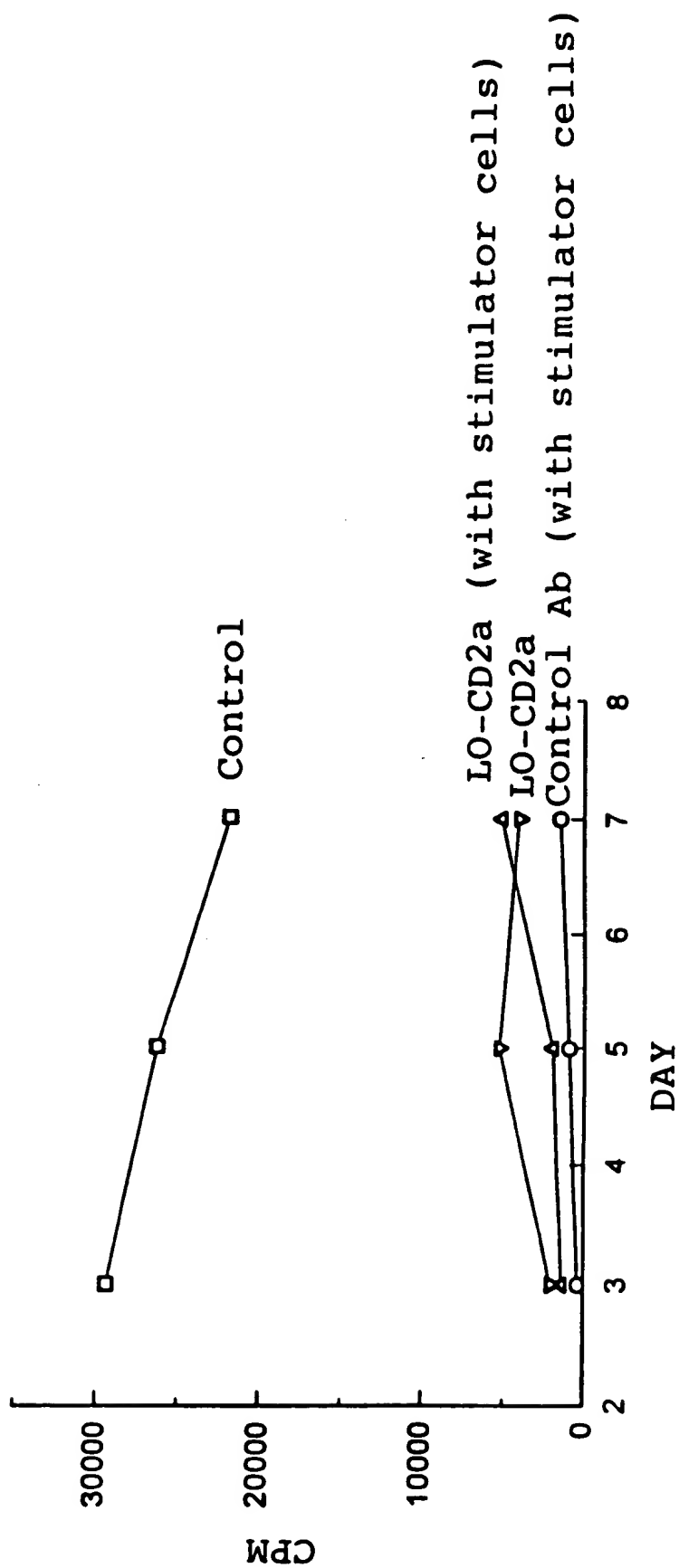
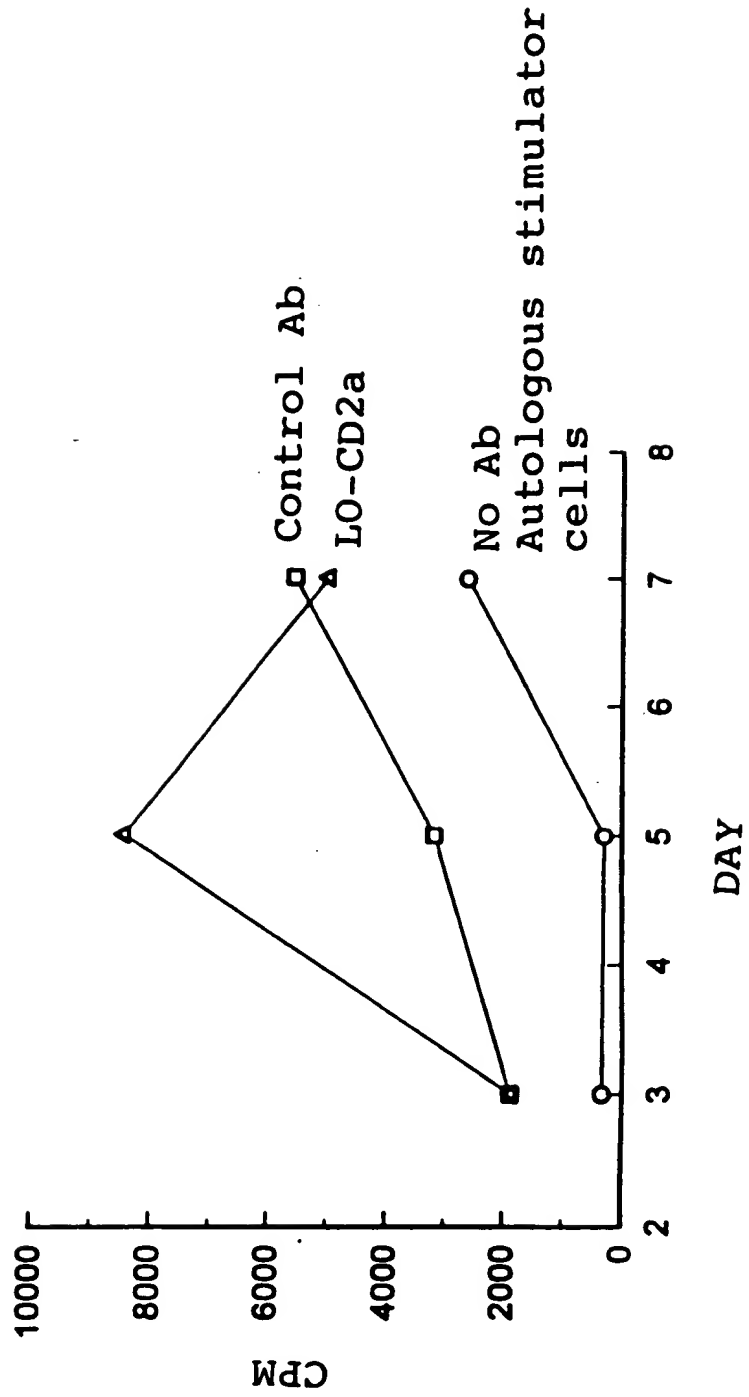


FIG. 38B



862040-2495060

52/53

FIG. 39

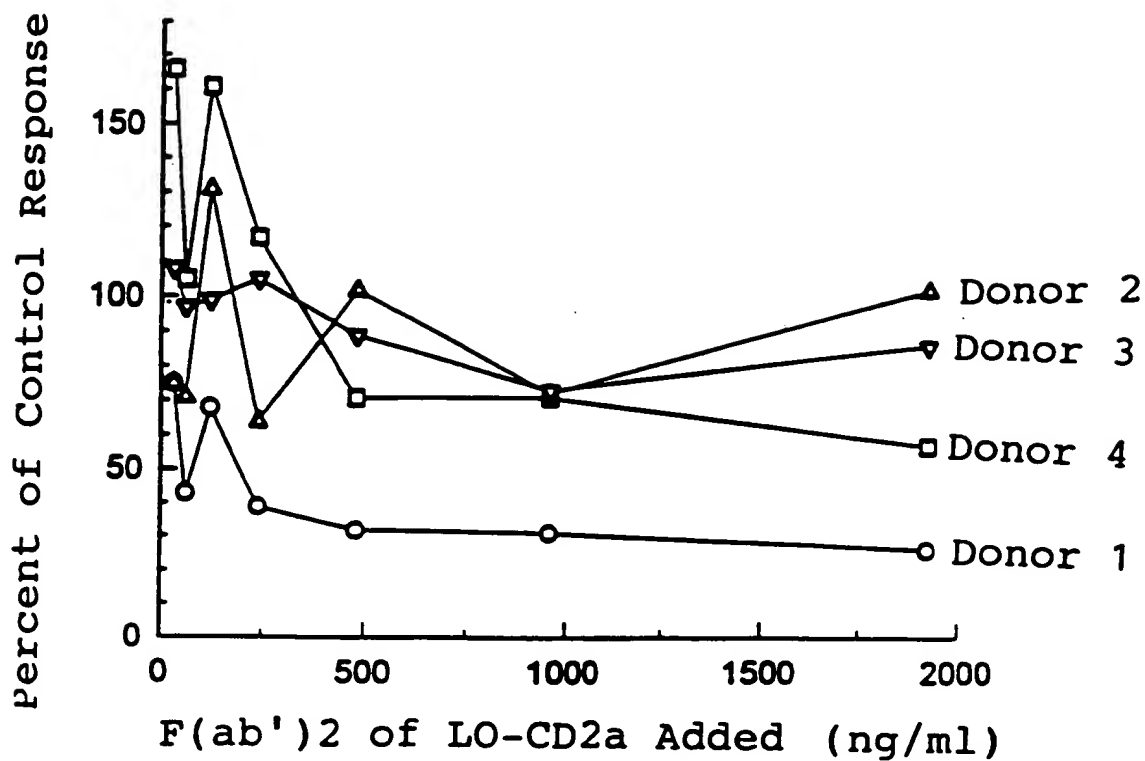


FIG. 40

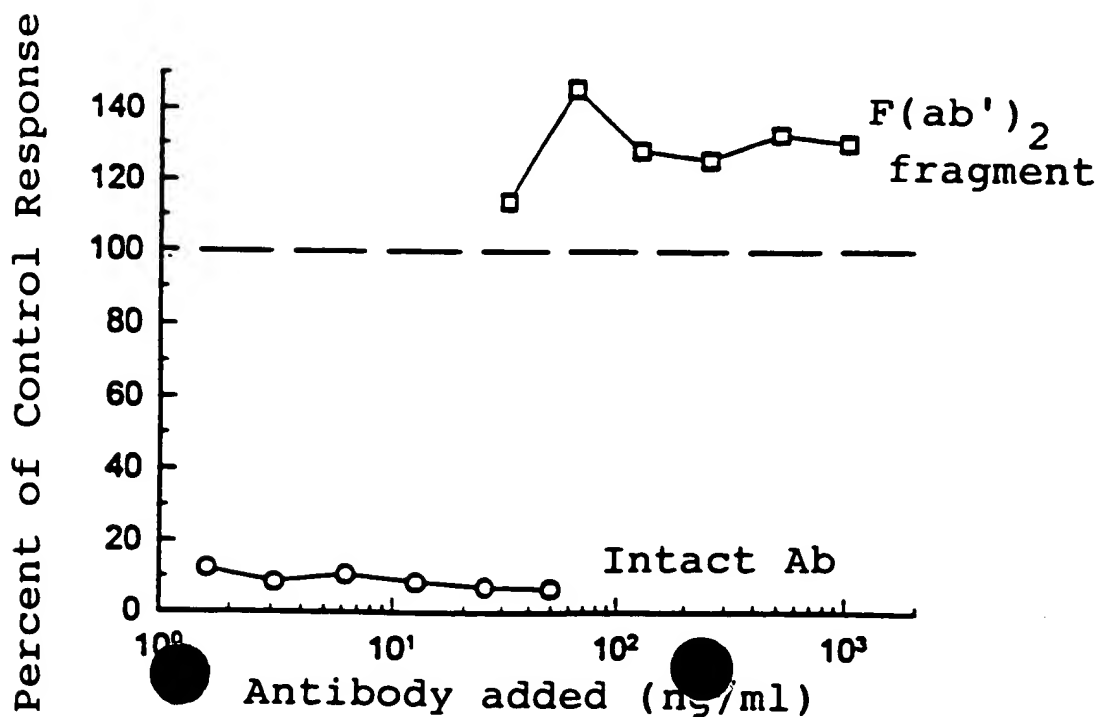


FIG. 41

